OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 17:47:08 ; Search time 18.4646 Seconds
(without alignments)
384.304 Million cell updates/sec

Title: US-10-774-076-14
Perfect Score: 561
Sequence: 1 DIQMTQSPSSLSASVGDRVT.........CLQYDEFPYTFGGGTKVEIK 107

Scoring table: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	510	90.9	107	2	US-08-290-592E-20	Sequence 20, Appl
2	510	90.9	107	5	PCT-US95-10053-17	Sequence 17, Appl
3	510	90.9	107	5	PCT-US96-09448-20	Sequence 20, Appl
4	502	89.5	107	1	US-08-107-669D-27	Sequence 27, Appl
5	502	89.5	107	1	US-08-472-788A-27	Sequence 27, Appl
6	502	89.5	107	1	US-08-477-531B-27	Sequence 27, Appl
7	502	89.5	107	2	US-08-082-842A-27	Sequence 27, Appl
8	499	88.9	107	4	US-09-647-468-107	Sequence 107, App
9	499	88.9	127	4	US-09-647-468-182	Sequence 182, App
10	498	88.8	107	1	US-08-425-336-125	Sequence 125, App
11	498	88.8	107	1	US-08-488-113B-125	Sequence 125, App
12	498	88.8	107	1	US-08-477-484B-125	Sequence 125, App
13	498	88.8	107	1	US-08-107-669D-65	Sequence 65, Appl
14	498	88.8	107	1	US-08-472-788A-87	Sequence 87, Appl
15	498	88.8	107	1	US-08-477-531B-65	Sequence 65, Appl
16	498	88.8	107	2	US-08-646-360-125	Sequence 125, Appl
17	498	88.8	107	2	US-08-082-842A-87	Sequence 87, Appl
18	498	88.8	107	3	US-08-839-765-125	Sequence 125, App
19	498	88.8	107	3	US-09-136-389-125	Sequence 125, App
20	498	88.8	107	4	US-09-610-838-125	Sequence 125, App
21	498	88.8	107	3	US-09-711-485-125	Sequence 125, App
22	495	88.2	240	1	US-08-488-113B-147	Sequence 147, App
23	495	88.2	240	1	US-08-488-113B-148	Sequence 148, App
24	495	88.2	240	1	US-08-477-484B-147	Sequence 147, App
25	495	88.2	240	1	US-08-477-484B-148	Sequence 148, App
26	495	88.2	240	2	US-08-646-360-147	Sequence 147, App
27	495	88.2	240	2	US-08-646-360-148	Sequence 148, App
28	495	88.2	240	3	US-08-839-765-147	Sequence 147, App
29	495	88.2	240	3	US-08-839-765-148	Sequence 148, App
30	495	88.2	240	3	US-09-136-389-147	Sequence 147, App
31	495	88.2	240	3	US-09-136-389-148	Sequence 148, App
32	495	88.2	240	3	US-09-711-485-148	Sequence 148, App
33	495	88.2	240	4	US-09-610-838-148	Sequence 148, App
34	495	88.2	240	3	US-09-711-485-147	Sequence 147, App
35	495	88.2	240	4	US-09-610-838-147	Sequence 147, App
36	493	87.9	107	4	US-09-647-468-99	Sequence 99, App
37	493	87.9	127	4	US-09-647-468-180	Sequence 180, App
38	491	87.5	355	3	US-08-875-811-41	Sequence 41, Appl
39	491	87.5	355	3	US-08-875-811-49	Sequence 49, Appl
40	491	87.5	355	3	US-08-875-811-64	Sequence 64, Appl
41	491	87.5	358	3	US-08-875-811-45	Sequence 45, Appl
42	491	87.5	358	3	US-08-875-811-51	Sequence 51, Appl
43	491	87.5	360	3	US-08-875-811-47	Sequence 47, Appl
44	491	87.5	379	3	US-08-875-811-43	Sequence 43, Appl
45	489	87.2	107	4	US-09-647-468-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-08-290-592E-20

Sequence 20, Application US/08290592E
Patent No. 5824307
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
; ADDRESSEE: OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,592E
; FILING DATE: August 15, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 469201-257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-290-592E-20

Query Match   90.9%; Score 510; DB 2; Length 107;
Best Local Similarity   88.8%;
Matches   95; Conservative   8; Mismatches   4; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTTTCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
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Db   1 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 60
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Qy  61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEPPYTFGGGTKVEIK 107
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Db  61 RFSGSGSGTEFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 107
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RESULT 2
PCT-US95-10053-17
; Sequence 17, Application PCT/US9510053
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytia
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; CLASSIFICATION:
; APPLICATION NUMBER: PCT/US95/10053
; FILING DATE: Concurrently
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,592
; FILING DATE: August 15, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 462201-274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; PCT-US95-10053-17

Query Match   90.9%; Score 510; DB 5; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.2e-44;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

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Db   1 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 60
Qy  61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEPPYTFGGGTKVEIK 107
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Db  61 RFSGSGSGTEFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 107
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RESULT 3
PCT-US96-09448-20
; Sequence 20, Application PC/TUS9609448
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Synctyica

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09448
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,592
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HERRON, CHARLES J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 462201-257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; PCT-US96-09448-20

Query Match   90.9%; Score 510; DB 5; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.2e-44;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

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Qy   1 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 60
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Db   1 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 60
Qy  61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEPPYTFGGGTKVEIK 107
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Db  61 RFSGSGSGTEFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 107
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RESULT 4
US-08-107-669D-27
; Sequence 27, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D

FILING DATE: 13-AUG-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 424
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/808,464
ATTORNEY/AGENT INFORMATION:
FILING DATE: 13-DEC-1991
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540

US-08-107-669D-27
MOLECULE TYPE: protein
TOPOLOGY: linear
TYPE: amino acid
LENGTH: 107 amino acids
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 27:

Query Match
Best Local Similarity 89.5%; Score 502; DB 1; Length 107;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Pred. No. 2.6e-43;

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Qy  1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
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Db  1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
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Db 61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107
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RESULT 5
US-08-472-788A-27
Sequence 27, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-27

Query Match
Best Local Similarity 89.5%; Score 502; DB 1; Length 107;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Pred. No. 2.6e-43;

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Qy  1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
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Db  1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
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Db 61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107
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RESULT 6
US-08-477-531B-27
Sequence 27, Application US/08477531B
Patent No. 5821123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 436
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
US-08-477-531B-27
MOLECULE TYPE: protein
TOPOLOGY: linear
TYPE: amino acid
LENGTH: 107 amino acids
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 27:

RESULT 7
US-08-082-842A-27
Sequence 27, Application US/08082842A
Patent No. 5869619
GENERAL INFORMATION:
;   APPLICANT: Studnicka, Gary M.
;   TITLE OF INVENTION: Modified Antibody Variable Domains
;   NUMBER OF SEQUENCES: 89
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
;   STREET: 1100 New York Ave., N.W., Suite 600
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20005-3934
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/082,842A
;   FILING DATE: 23-JUN-1993
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/10906
;   FILING DATE: 14-DEC-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/808,464
;   FILING DATE: 13-DEC-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Cimbala, Michele A.
;   REGISTRATION NUMBER: 33,851
;   REFERENCE/DOCKET NUMBER: 0610.1000002
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202/371-2600
;   TELEFAX: 202/371-2540
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 27:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein

  Query Match   89.5%; Score 502; DB 2; Length 107;
  Best Local Similarity   88.8%; Pred. No. 2.6e-43;
  Matches   95; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
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Db 1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYEDFPYTFGGGTKVEIK 107
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Db 61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

US-09-647-468-107
Sequence 107, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
;   APPLICANT: SATO, KOH
;   APPLICANT: ADACHI, HIDEKI
;   APPLICANT: YABUTA, NAOHIRO
;   TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;   TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;   FILE REFERENCE: 053466/0289
;   CURRENT APPLICATION NUMBER: US/09/647,468
;   CURRENT FILING DATE: 2000-09-29
;   PRIOR APPLICATION NUMBER: PCT/JP99/01768
;   PRIOR FILING DATE: 1999-04-02
;   PRIOR APPLICATION NUMBER: JP 10-91850
;   PRIOR FILING DATE: 1998-04-03
;   NUMBER OF SEQ ID NOS: 183
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 107
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence coding of version "b1" of humanized L
;   OTHER INFORMATION: chain V region
US-09-647-468-107

  Query Match   88.9%; Score 499; DB 4; Length 107;
  Best Local Similarity   89.7%; Pred. No. 5.3e-43;
  Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
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Db 1 DIQMTQSPSSLSASVGDRVTITCRASQDIKSFLSWFQQKPGKSPKTLIYATSLADGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||| ||||||||||||||||||||: |||:|||||||||||
Db 61 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 107

RESULT 9
US-09-647-468-182
Sequence 182, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
;   APPLICANT: SATO, KOH
;   APPLICANT: ADACHI, HIDEKI
;   APPLICANT: YABUTA, NAOHIRO
;   TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;   TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;   FILE REFERENCE: 053466/0289
;   CURRENT APPLICATION NUMBER: US/09/647,468
;   CURRENT FILING DATE: 2000-09-29
;   PRIOR APPLICATION NUMBER: PCT/JP99/01768
;   PRIOR FILING DATE: 1999-04-02
;   PRIOR APPLICATION NUMBER: JP 10-91850
;   PRIOR FILING DATE: 1998-04-03
;   NUMBER OF SEQ ID NOS: 183
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 182
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence coding of version "b1" of humanized H
;   OTHER INFORMATION: chain V region
US-09-647-468-182

  Query Match   88.9%; Score 499; DB 4; Length 127;
  Best Local Similarity   89.7%; Pred. No. 6.5e-43;
  Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

RESULT 8
US-08-082-842A-27

  Query Match   89.5%; Score 502; DB 2; Length 107;
  Best Local Similarity   88.8%; Pred. No. 2.6e-43;
  Matches   95; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       ||||||||||:|||:||||||||:|||||||||||||||||| :|||||||||||||||||
Db 1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||| |||||||||| |||:|||||:| |||:|||||||:|||
Db 61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

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Qy        1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
            ||||||||||||||||||||||||||||| :|| ||||||||:|||||| : :|:|||||
Db       21 DIQMTQSPSSLSASVGDRVTITCKASQDIKSFLSWFQQKPGKSPKTLIYAISIADGVPS 80

Qy       61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            ||||||||:||||||||||||||||||||:| ::| |||||||||||
Db       81 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 127
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RESULT 10
US-08-425-336-125
; Sequence 125, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-125

Query Match   88.8%; Score 498; DB 1; Length 107;
Best Local Similarity   89.7%; Pred. No. 6.7e-43;
Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

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Qy        1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
            |||||||||||||||||||||||:||||||||||||||||||||||||||||||  |||||
Db        1 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS 60

Qy       61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            ||||||||:|||||||||:||:|| ::||| ||:: |||||||:|||
Db       61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107
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RESULT 11
US-08-488-113B-125
; Sequence 125, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-125

Query Match   88.8%; Score 498; DB 1; Length 107;
Best Local Similarity   89.7%; Pred. No. 6.7e-43;
Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

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Qy        1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
            |||||||||||||||||||||||:|||||||||||||||||||||||||||||| |||||
Db        1 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS 60

Qy       61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            ||||||||:|||||||||:||:|| ::||| ||:: |||||||:|||
Db       61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107
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RESULT 12
US-08-477-484B-125
; Sequence 125, Application US/0847748B
; Patent No. 5756699
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;   APPLICANT: Carroll, Stephen F.
;   APPLICANT: Studnika, Gary M.
;   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;   TITLE OF INVENTION: Proteins
;   NUMBER OF SEQUENCES: 169
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;   STREET: 500 West Madison Street, 34th floor
;   CITY: Chicago.
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60661
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/477,484B
;   FILING DATE: 07-JUN-1995
;   PRIOR APPLICATION DATA:
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/425,336
;   FILING DATE: 18-APR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/064,691
;   FILING DATE: 12-MAY-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/988,430
;   FILING DATE: 09-DEC-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/901,707
;   FILING DATE: 19-JUN-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/787,567
;   FILING DATE: 04-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McNicholas, Janet M.
;   REGISTRATION NUMBER: 32,918
;   REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312/707-8889
;   TELEFAX: 312/707-9155
;   TELEX: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 125:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-477-484B-125

  Query Match   88.8%; Score 498; DB 1; Length 107;
  Best Local Similarity   89.7%; Pred. No. 6.7e-43;
  Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||||:||||||||:||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
          ||||||||||||||||||||||||||||||||||||||:||:||||||
Db   61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 13
US-08-107-669D-65
; Sequence 65, Application US/0810769D
; Patent No. 5766886
; GENERAL INFORMATION:
;   APPLICANT: Studnicka, Gary M.
;   TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
;   NUMBER OF SEQUENCES: 67
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
;   STREET: 1100 New York Ave., N.W., Suite 600
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: United States of America
;   ZIP: 20005-3934
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/107,669D
;   FILING DATE: 13-AUG-1993
;   PRIOR APPLICATION DATA:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/10906
;   FILING DATE: 14-DEC-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/808,464
;   FILING DATE: 13-DEC-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Michele A. Cimbala
;   REGISTRATION NUMBER: 33,851
;   REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202/371-2600
;   TELEFAX: 202/371-2540
;   INFORMATION FOR SEQ ID NO: 65:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-107-669D-65

  Query Match   88.8%; Score 498; DB 1; Length 107;
  Best Local Similarity   89.7%; Pred. No. 6.7e-43;
  Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||||:||||||||:||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
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Db   61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 14
US-08-472-788A-87
; Sequence 87, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
;   APPLICANT: Studnicka, Gary M.
;   TITLE OF INVENTION: Modified Antibody Variable Domains
;   NUMBER OF SEQUENCES: 89
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
;   STREET: 1100 New York Ave., N.W., Suite 600
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20005-3934

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,788A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/082,842
 FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
 NAME: Cimbala, Michele A.
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/371-2600
 TELEFAX: 202/371-2540
US-08-472-788A-87

INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match   88.8%; Score 498; DB 1; Length 107;
Best Local Similarity   89.7%; Pred. No. 6.7e-43;
Matches 96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

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Qy  1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
        ||||||||||||||||||||||:|||||||||||||||||||||||||||||    |||
Db  1 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
        ||||||||  ||||||||||  ||  |||||    |||||||||  ||
Db 61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDBSPWTFGGGTKLEIK 107
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RESULT 15
US-08-477-531B-65
Sequence 65, Application US/0847531B
Patent No. 5821123
GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
 NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
 STREET: 1100 New York Ave., N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20005-3934
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,531B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 436
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/107,669

FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
 NAME: Michele A. Cimbala
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/371-2600
 TELEFAX: 202/371-2540
US-08-477-531B-65

INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match   88.8%; Score 498; DB 2; Length 107;
Best Local Similarity   89.7%; Pred. No. 6.7e-43;
Matches 96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

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Qy  1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
        ||||||||||||||||||||||:|||||||||||||||||||||||||||||    |||
Db  1 DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
        ||||||||  ||||||||||  ||  |||||    |||||||||  ||
Db 61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDBSPWTFGGGTKLEIK 107
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Search completed: December 29, 2004, 18:09:14
Job time : 19.4646 secs

OM protein - protein search, using sw model

; Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

Run on: December 29, 2004, 17:47:08 ; Search time 20.5354 Seconds
                                                  (without alignments)
                                                  384.304 Million cell updates/sec

Title: US-10-774-076-2
Perfect Score: 648
Sequence: 1 EIQLQQSGPELVKPGASVKV..........GNFPYYFDYWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Issued_Patents_AA:*
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    2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
    3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
    4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
    5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
    6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560.5	86.5	118	4	US-09-647-468-139	Sequence 139, App
2	560.5	86.5	118	4	US-09-647-468-140	Sequence 140, App
3	560.5	86.5	137	4	US-09-647-468-153	Sequence 153, App
4	560.5	86.5	137	4	US-09-647-468-154	Sequence 154, App
5	529.5	81.7	116	2	US-08-273-146-55	Sequence 55, Appl
6	512.5	79.1	116	4	US-09-647-468-144	Sequence 144, App
7	512.5	79.1	137	4	US-09-647-468-158	Sequence 158, App
8	512.5	78.6	135	1	US-08-137-117D-27	Sequence 27, Appl
9	509.5	78.6	135	1	US-08-436-717-27	Sequence 27, Appl
10	503.5	77.7	116	2	US-08-672-345C-105	Sequence 105, Appl
11	503.5	77.7	116	3	US-09-214-095D-90	Sequence 90, Appl
12	503.5	77.7	118	4	US-09-647-468-143	Sequence 143, App
13	503.5	77.7	118	4	US-09-647-468-157	Sequence 157, App
14	498.5	76.9	116	2	US-08-672-345C-14	Sequence 14, Appl
15	498.5	76.9	116	3	US-09-214-095D-14	Sequence 14, Appl
16	495.5	76.5	116	2	US-08-672-345C-106	Sequence 106, Appl
17	494.5	76.3	137	2	US-08-116-778E-3	Sequence 3, Appl
18	494.5	76.3	137	2	US-08-438-562-3	Sequence 3, Appl
19	494.5	76.3	137	2	US-08-483-528B-93	Sequence 93, Appl
20	494.5	76.3	139	2	US-08-116-778E-1	Sequence 1, Appli
21	494.5	76.3	139	2	US-08-438-562-1	Sequence 1, Appli
22	494.5	76.3	139	2	US-08-483-528B-91	Sequence 91, Appli
23	492	75.9	117	4	US-08-814-806-4	Sequence 4, Appli
24	492	75.9	117	4	US-09-293-854-4	Sequence 4, Appli
25	490.5	75.7	116	4	US-07-634-278-56	Sequence 56, Appl
26	490.5	75.7	116	1	US-08-477-728-56	Sequence 56, Appl
27	490.5	75.7	116	1	US-08-474-040-56	Sequence 56, Appl
28	490.5	75.7	116	1	US-08-487-200-56	Sequence 56, Appl
29	490.5	75.7	116	1	US-08-484-537-56	Sequence 56, Appl
30	490.5	75.7	135	1	US-07-634-278-69	Sequence 69, Appl
31	490.5	75.7	135	1	US-08-477-728-69	Sequence 69, Appl
32	490.5	75.7	135	1	US-08-474-040-69	Sequence 69, Appl
33	490.5	75.7	135	1	US-08-487-200-69	Sequence 69, Appl
34	490.5	75.7	135	1	US-08-484-537-69	Sequence 69, Appl
35	490	75.6	130	4	US-09-556-605-3	Sequence 3, Appli
36	488.5	75.4	297	4	US-09-486-814A-2	Sequence 2, Appli
37	484	74.7	137	1	US-08-482-882-43	Sequence 43, Appl
38	484	74.7	137	2	US-08-483-389-43	Sequence 43, Appl
39	484	74.7	137	2	US-08-473-503-43	Sequence 43, Appl
40	484	74.7	137	2	US-08-487-1113D-43	Sequence 43, Appl
41	484	74.7	137	2	US-08-720-420A-43	Sequence 43, Appl
42	484	74.7	137	2	US-08-483-932-43	Sequence 43, Appl
43	484	74.7	137	3	US-08-714-017-43	Sequence 43, Appl
44	484	74.7	137	3	US-08-475-680-43	Sequence 43, Appl
45	482	74.4	118	4	US-09-802-083-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-647-468-139
; Sequence 139, Application US/0964746B
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 139
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-139

Query Match   86.5%; Score 560.5; DB 4; Length 118;
Best Local Similarity   89.9%; Pred. No. 1.1e-46;
Matches 107; Conservative   4; Mismatches   7; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVTYCARRGNFPYYFDYWGQGTTLTVSS 119
             |.|||.|||||||||||||||:||||||||||||||||| |||||||||||||||
Db   61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVTYCARGGB-GYYFDYWGQGTTLTVSS 118

RESULT 2
US-09-647-468-140
; Sequence 140, Application US/0964746B
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

```
;  TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0289
;  CURRENT APPLICATION NUMBER: US/09/647,468
;  CURRENT FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: PatentIn Ver. 2.1
;
;  SEQ ID NO 140
;  LENGTH: 118
;  TYPE: PRT
;  ORGANISM: Mus sp.
;  FEATURE:
;  OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
US-09-647-468-140

Qy         1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1  EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY   60

Qy        61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVSS  119
              :||||||||||||||||||||||||||||||||||||||:|||||||| |||||||||||
Db        61  NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLTVSS  118
```

```
RESULT 3
US-09-647-468-153
;  Sequence 153, Application US/09647468
;  Patent No. 6677436
;  GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: ADACHI, HIDEKI
;  APPLICANT: YABUTA, NAOHIRO
;  TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;  TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0289
;  CURRENT APPLICATION NUMBER: US/09/647,468
;  CURRENT FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: PatentIn Ver. 2.1
;
;  SEQ ID NO 153
;  LENGTH: 137
;  TYPE: PRT
;  ORGANISM: Mus sp.
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;  OTHER INFORMATION: sequence coding for H chain V region of ant-TF
US-09-647-468-153

Query Match            86.5%;  Score 560.5;  DB 4;  Length 137;
Best Local Similarity  89.9%;  Pred. No. 1.3e-46;
Matches 107;  Conservative   4;  Mismatches    7;  Indels    1;  Gaps    1;
```

```
;  TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0289
;  CURRENT APPLICATION NUMBER: US/09/647,468
;  CURRENT FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: PatentIn Ver. 2.1
;
;  SEQ ID NO 154
;  LENGTH: 137
;  TYPE: PRT
;  ORGANISM: Mus sp.
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;  OTHER INFORMATION: sequence coding for H chain V region of anti-TF
US-09-647-468-154

RESULT 4
US-09-647-468-154
;  Sequence 154, Application US/09647468
;  Patent No. 6677436
;  GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: ADACHI, HIDEKI
;  APPLICANT: YABUTA, NAOHIRO
;  TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
```

```
Qy         1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1  EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY   60

Qy        61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVSS  119
              :||||||||||||||||||||||||||||||||||||||:||||||||  |||||||||||
Db        80  NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLTVSS  137
```

```
Query Match            86.5%;  Score 560.5;  DB 4;  Length 137;
Best Local Similarity  89.9%;  Pred. No. 1.3e-46;
Matches 107;  Conservative   4;  Mismatches    7;  Indels    1;  Gaps    1;
```

```
RESULT 5
US-08-273-146-55
;  Sequence 55, Application US/08273146
;  Patent No. 5855885
;  GENERAL INFORMATION:
;  APPLICANT: Smith, Rodger
;  APPLICANT: McCafferty, John
;  APPLICANT: Chiswell, David
;  APPLICANT: Darsley, Michael J.
;  APPLICANT: Fitzgerald, Kevin
;  APPLICANT: Kenten, John H.
;  APPLICANT: Martin, Mark T.
;  APPLICANT: Titmas, Richard C.
;  APPLICANT: Williams, Richard O.
;  TITLE OF INVENTION: The Isolation and Production of
;  TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
;  NUMBER OF SEQUENCES: 71
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: IGEN, Inc.
;  STREET: 1530 East Jefferson St.
;  CITY: Rockville
;  STATE: MD
;  COUNTRY: USA
;  ZIP: 20852
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
```

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Qy         1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        20  EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY   79

Qy        61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVSS  119
              :||||||||||||||||||||||||||||||||||||||:|||||||| |||||||||||
Db        80  NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLTVSS  137
```

```
Query Match            86.5%;  Score 560.5;  DB 4;  Length 137;
Best Local Similarity  89.9%;  Pred. No. 1.3e-46;
Matches 107;  Conservative   4;  Mismatches    7;  Indels    1;  Gaps    1;
```

```
;  APPLICATION NUMBER: US/08/273,146
;  FILING DATE: 14-JUL-1994
;  CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Ryan, John W.
;  REGISTRATION NUMBER: 33,771
;  REFERENCE/DOCKET NUMBER: 09000
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 301-984-8000
;  TELEFAX: 301-230-0158
;  INFORMATION FOR SEQ ID NO: 55:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 116 amino acids
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-273-146-55
```

```
Query Match    81.7%;  Score 529.5;  DB 2;  Length 116;
Best Local Similarity  85.7%;  Pred. No. 1e-43;
Matches 102;  Conservative  6;  Mismatches  8;  Indels  3;  Gaps  2;

Qy   1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY  60
        :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   1  QVQLQQSGPELVKPGASVKVSCKASGYAFTNYNIYWVKQSHGKSLEWIGYIDPYSGGSSY  60

Qy  61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFPYYFDYWGQGTTLTVSS  119
        :||||||||||||||||||||||||||| |||||||||| : ||||||||||||||||
Db  61  NQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCA--GGNP-RFAFWGQGTTLVTVSS  116
```

RESULT 6
```
US-09-647-468-144
;  Sequence 144, Application US/09647468
;  Patent No. 6677436
;  GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: ADACHI, HIDEKI
;  APPLICANT: YABUTA, NAOHIRO
;  TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;  TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0289
;  CURRENT APPLICATION NUMBER: US/09/647,468
;  CURRENT FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 144
;  LENGTH: 118
;  TYPE: PRT
;  ORGANISM: Mus sp.
;  FEATURE:
;  OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse
US-09-647-468-144
```

```
Query Match    79.1%;  Score 512.5;  DB 4;  Length 118;
Best Local Similarity  81.7%;  Pred. No. 4.4e-42;
Matches 98;  Conservative  10;  Mismatches  9;  Indels  3;  Gaps  2;

Qy   1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY  60
        :|||||||||||||||||||||||||| ||||||||||||||||||||||||||:
Db   1  DIQLQQSGPELVKPGASVKVSCKASGYSFTDYNIFWVKQSHGKSLEWIGYIDPYTGGTGY  60

Qy  61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFPYYFD-YWGQGTTLTVSS  119
        :||| ||||||||||||||||||||||||||||||||||| : ||||: :|||:
Db  61  NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCAR--GFYYDYDCYWGQGTLVTVSA  118
```

RESULT 7

```
US-09-647-468-158
;  Sequence 158, Application US/09647468
;  Patent No. 6677436
;  GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: ADACHI, HIDEKI
;  APPLICANT: YABUTA, NAOHIRO
;  TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;  TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0289
;  CURRENT APPLICATION NUMBER: US/09/647,468
;  CURRENT FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 158
;  LENGTH: 137
;  TYPE: PRT
;  ORGANISM: Mus sp.
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
;  OTHER INFORMATION: sequence coding for H chain V region of ant-TF
;  OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-158
```

```
Query Match    79.1%;  Score 512.5;  DB 4;  Length 137;
Best Local Similarity  81.7%;  Pred. No. 5.3e-42;
Matches 98;  Conservative  10;  Mismatches  9;  Indels  3;  Gaps  2;

Qy   1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY  60
        :|||||||||||||||||||||||||| ||||||||||||||||||||||||||:   | |
Db  20  DIQLQQSGPELVKPGASVKVSCKASGYSFTDYNIFWVKQSHGKSLEWIGYIDPYTGGTGY  79

Qy  61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFPYYFD-YWGQGTTLTVSS  119
        :||| ||||||||||||||||||||||||||||||||||| : ||||: :|||:
Db  80  NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCAR--GFYYDYDCYWGQGTLVTVSA  137
```

RESULT 8
```
US-08-137-117D-27
;  Sequence 27, Application US/08137117D
;  Patent No. 5795965
;  GENERAL INFORMATION:
;  APPLICANT: TSUCHIYA, Masayuki
;  APPLICANT: SATO, Koh
;  APPLICANT: BENDIG, Mary
;  APPLICANT: JONES, Steven
;  APPLICANT: SALDANHA, Jose
;  TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;  TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
;  NUMBER OF SEQUENCES: 158
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Foley & Lardner
;  STREET: 3000 K Street, N.W., Suite 500
;  CITY: Washington
;  STATE: D.C.
;  COUNTRY: USA
;  ZIP: 20007-5109
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: Patentin Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/137,117D
;  FILING DATE: 20-DEC-1993
;  CLASSIFICATION: 530
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: WO PCT/JP92/00544
;  FILING DATE: 24-APR-1992
```

PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 4-32084
  FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 3-95476
  FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
  NAME: WEGNER, Harold C.
  REGISTRATION NUMBER: 25,258
  REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202)672-5300
  TELEFAX: (202)672-5399
  TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 135 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-137-117D-27

Query Match   78.6%;   Score 509.5; DB 1; Length 135;
Best Local Similarity 80.7%; Pred. No. 1e-41;
Matches 96; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

```
Qy   1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20  EIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSHGKSLEWIGYIDPFNGGTSY 79

Qy  61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
        :|||||||||||||||||:| ||||||||||||||||||| ||||||| |||| :|||:
Db  80  NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGGN---RFAYWGQGTLVTVSA 135
```

RESULT 9
US-08-436-717-27
Sequence 27, Application US/0836717
Patent No. 5817790
GENERAL INFORMATION:
  APPLICANT: TSUCHIYA, Masayuki
  APPLICANT: SATO, Koh
  APPLICANT: BENDIG, Mary
  APPLICANT: JONES, Steven
  APPLICANT: SALDANHA, Jose
  TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
  TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
  NUMBER OF SEQUENCES: 158
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Foley & Lardner
  STREET: 3000 K Street, N.W., Suite 500
  CITY: Washington
  STATE: D.C.
  COUNTRY: USA
  ZIP: 20007-5109
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/436,717
  FILING DATE:
  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/137,117
  FILING DATE: 20-DEC-1993
  APPLICATION NUMBER: WO PCT/JP92/00544
  FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 4-32084
  FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476
  FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
  NAME: WEGNER, Harold C.
  REGISTRATION NUMBER: 25,258
  REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202)672-5300
  TELEFAX: (202)672-5399
  TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 135 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-436-717-27

Query Match   78.6%;   Score 509.5; DB 2; Length 135;
Best Local Similarity 80.7%; Pred. No. 1e-41;
Matches 96; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

```
Qy   1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20  EIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSHGKSLEWIGYIDPFNGGTSY 79

Qy  61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
        :|||||||||||||||||:| ||||||||||||||||||| ||||||| |||| :|||:
Db  80  NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCARGGN---RFAYWGQGTLVTVSA 135
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RESULT 10
US-08-672-345C-105
Sequence 105, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
  APPLICANT: Landry Donald, W.
  TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
  NUMBER OF SEQUENCES: 108
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Cooper and Dunham LLP
  STREET: 1185 Avenue of the Americas
  CITY: New York
  STATE: New York
  COUNTRY: USA
  ZIP: 10036
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/672,345C
  FILING DATE: 24-JUN-1996
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  NAME: White, John P.
  REGISTRATION NUMBER: 28,678
  REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 212-278-0400
  TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 105:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 116 amino acids
  TYPE: amino acid
  STRANDEDNESS: Single
  TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
US-08-672-345C-105

Query Match   77.7%;   Score 503.5; DB 2; Length 116;
Best Local Similarity 79.8%; Pred. No. 3.2e-41;

```
Matches 95; Conservative 11; Mismatches 10; Indels 3; Gaps 1;

Qy  1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
       |||:||||||||||||||:||||||:||||:||||||||||||||||||||:| |||:
Db  1 EIHLQQSGPELVKPGASVKLSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPHNGGIFY 60

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGGGTTLTVSS 119
       .|||||.||||||||.:|.||||||||||||||||||    ||:|  ||:|.|||:
Db 61 NQKFKGRATLTVDKSSNTAFMHLNSLTSEDSAVYYCARGGGL---PAYWGRGTLVTVSA 116
```

RESULT 11
US-09-214-095D-90
; Sequence 90, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
;   APPLICANT: Landry, Donald
;   TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
;   FILE REFERENCE: 51400-A-PCT-US
;   CURRENT APPLICATION NUMBER: US/09/214,095D
;   CURRENT FILING DATE: 1999-07-19
;   NUMBER OF SEQ ID NOS: 121
;   SOFTWARE: Patentin version 3.0
; SEQ ID NO 90
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Murine
US-09-214-095D-90

Query Match   77.7%; Score 503.5; DB 3; Length 116;
Best Local Similarity   79.8%; Pred. No. 3.2e-41;
Matches 95; Conservative 11; Mismatches 10; Indels   3; Gaps   1;

```
Qy  1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60

Db  1 EIHLQQSGPELVKPGASVKLSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPHNGGIFY 60

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGGGTTLTVSS 119

Db 61 NQKFKGRATLTVDKSSNTAFMHLNSLTSEDSAVYYCARGGGL---PAYWGRGTLVTVSA 116
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RESULT 12
US-09-647-468-143
; Sequence 143, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
;   APPLICANT: SATO, KOH
;   APPLICANT: ADACHI, HIDEKI
;   APPLICANT: YABUTA, NAOHIRO
;   TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;   TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;   FILE REFERENCE: 053466/0289
;   CURRENT APPLICATION NUMBER: US/09/647,468
;   CURRENT FILING DATE: 2000-09-29
;   PRIOR APPLICATION NUMBER: PCT/JP99/01768
;   PRIOR FILING DATE: 1999-04-02
;   PRIOR APPLICATION NUMBER: JP 10-91850
;   PRIOR FILING DATE: 1998-04-03
;   NUMBER OF SEQ ID NOS: 183
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 143
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse
;   OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-143

Query Match   80.0%; Score 503.5; DB 4; Length 118;
Best Local Similarity   80.0%; Pred. No. 3.2e-41;
Matches 96; Conservative 11; Mismatches 10; Indels   3; Gaps   2;

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Qy  1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60

Db  1 DIQLQQSGPELVKPGGSSVKVSCKASGYSFTDYNIFWVKQSHGKSLEWIGYIDPYYGGTGY 60

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFD-YWGQGTTLTVSS 119

Db 61 NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCAR--GFYYDYCYWGQGTLVTVSA 118
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RESULT 13
US-09-647-468-157
; Sequence 157, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
;   APPLICANT: SATO, KOH
;   APPLICANT: ADACHI, HIDEKI
;   APPLICANT: YABUTA, NAOHIRO
;   TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;   TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;   FILE REFERENCE: 053466/0289
;   CURRENT APPLICATION NUMBER: US/09/647,468
;   CURRENT FILING DATE: 2000-09-29
;   PRIOR APPLICATION NUMBER: PCT/JP99/01768
;   PRIOR FILING DATE: 1999-04-02
;   PRIOR APPLICATION NUMBER: JP 10-91850
;   PRIOR FILING DATE: 1998-04-03
;   NUMBER OF SEQ ID NOS: 183
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 157
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence coding for H chain V region of anti-TF
;   OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-157

Query Match   77.7%; Score 503.5; DB 4; Length 137;
Best Local Similarity   80.0%; Pred. No. 3.9e-41;
Matches 96; Conservative 11; Mismatches 10; Indels   3; Gaps   2;

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Qy  1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60

Db 20 DIQLQQSGPELVKPGGSSVKVSCKASGYSFTDYNIFWVKQSHGKSLEWIGYIDPYYGGTGY 79

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFD-YWGQGTTLTVSS 119

Db 80 NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCAR--GFYYDYCYWGQGTLVTVSA 137
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RESULT 14
US-08-672-345C-14
; Sequence 14, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
;   APPLICANT: Landry, Donald, W.
;   TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
;   NUMBER OF SEQUENCES: 108
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Cooper and Dunham LLP
;   STREET: 1185 Avenue of the Americas
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10036
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:

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;  APPLICATION NUMBER: US/08/672,345C
;  FILING DATE: 24-JUN-1996
;  CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;  NAME: White, John P.
;  REGISTRATION NUMBER: 28,678
;  REFERENCE/DOCKET NUMBER: 0575/51400
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 212-278-0400
;  TELEFAX: 212-391-0525
;  INFORMATION FOR SEQ ID NO: 14:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH: 116 amino acids
;  TYPE: amino acid
;  STRANDEDNESS: single
;  TOPOLOGY: linear
;  MOLECULE TYPE: protein
US-08-672-345C-14

Query Match              76.9%;  Score 498.5;  DB 2;  Length 116;
Best Local Similarity    79.7%;  Pred. No. 9.6e-41;
Matches   94;  Conservative 10;  Mismatches 11;  Indels  3;  Gaps  1;

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Db     1  DVQLQESGPELVKPGASVKLSCKASGYPFTDYNMYWVKQSHGKSLEWIGYIDPSNGGIFY  60

Qy    61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVS  118
          :||||||:|||||||||||:|||||||||||||||||||||  :|||
Db    61  NQKFKGRATLTVDKSSNTAFMHLNSLTSEDSAVYYCARGGGL---FAYWGQGTLVTVS  115

RESULT 15
US-09-214-095D-14
;  Sequence 14, Application US/09214095D
;  Patent No. 6280987
;  GENERAL INFORMATION:
;  APPLICANT: Landry, Donald
;  TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
;  FILE REFERENCE: 51400-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/09/214,095D
;  CURRENT FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: PatentIn version 3.0
;  SEQ ID NO 14
;  LENGTH: 116
;  TYPE: PRT
;  ORGANISM: Murinae gen. sp.
US-09-214-095D-14

Query Match              76.9%;  Score 498.5;  DB 3;  Length 116;
Best Local Similarity    79.7%;  Pred. No. 9.6e-41;
Matches   94;  Conservative 10;  Mismatches 11;  Indels  3;  Gaps  1;

Qy     1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY  60
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Db     1  DVQLQESGPELVKPGASVKLSCKASGYPFTDYNMYWVKQSHGKSLEWIGYIDPSNGGIFY  60

Qy    61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVS  118
          :||||||:|||||||||||:|||||||||||||||||||||  :|||
Db    61  NQKFKGRATLTVDKSSNTAFMHLNSLTSEDSAVYYCARGGGL---FAYWGQGTLVTVS  115
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Search completed: December 29, 2004, 18:08:58
Job time : 22.5354 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 17:47:08 ; Search time 20.5354 Seconds
(without alignments)
384.304 Million cell updates/sec

Title: US-10-774-076-12
Perfect score: 642
Sequence: 1 EVQLVQSGAEVKKPGASVKI.........GNFPYFDYWGQGTLVTVSS 119
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Issued Patents AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	497.5	77.5	135	2	US-08-137-117D-102	Sequence 102, App
2	497.5	77.5	135	2	US-08-436-717-102	Sequence 102, App
3	496.5	77.3	116	1	US-08-561-521-41	Sequence 41, Appl
4	496.5	77.3	116	5	PCT-US95-01219-41	Sequence 41, Appl
5	491.5	76.6	135	1	US-08-137-117D-100	Sequence 100, App
6	491.5	76.6	135	2	US-08-436-717-100	Sequence 100, App
7	488.5	76.1	116	2	US-07-634-278-57	Sequence 57, Appl
8	488.5	76.1	116	3	US-07-634-278-73	Sequence 73, Appl
9	488.5	76.1	116	1	US-08-477-728-57	Sequence 57, Appl
10	488.5	76.1	116	1	US-08-477-728-73	Sequence 73, Appl
11	488.5	76.1	116	1	US-08-474-040-57	Sequence 57, Appl
12	488.5	76.1	116	1	US-08-474-040-73	Sequence 73, Appl
13	488.5	76.1	116	1	US-08-487-200-57	Sequence 57, Appl
14	488.5	76.1	116	1	US-08-487-200-73	Sequence 73, Appl
15	488.5	76.1	116	1	US-08-484-537-57	Sequence 57, Appl
16	488.5	76.1	116	3	US-08-484-537-73	Sequence 73, Appl
17	488.5	76.1	116	2	US-07-634-278-57	Sequence 57, Appl
18	483.5	75.3	116	1	US-08-477-728-5	Sequence 5, Appl
19	483.5	75.3	116	1	US-08-474-040-5	Sequence 5, Appl
20	483.5	75.3	116	1	US-08-487-200-5	Sequence 5, Appl
21	483.5	75.3	116	1	US-08-484-537-5	Sequence 5, Appl
22	483.5	75.3	116	1	US-08-477-484B-169	Sequence 169, App
23	483.5	75.3	116	1	US-08-107-669D-55	Sequence 55, Appl
24	483.5	75.3	116	1	US-08-472-788A-86	Sequence 86, Appl
25	483.5	75.3	116	1	US-08-477-531B-55	Sequence 55, Appl
26	483.5	75.3	116	2	US-08-646-169	Sequence 169, App
27	483.5	75.3	116	2	US-08-082-842A-86	Sequence 86, Appl
28	483.5	75.3	116	3	US-08-934-841-1	Sequence 1, Appli
29	483.5	75.3	116	3	US-09-393-409-1	Sequence 1, Appli
30	483.5	75.3	116	3	US-08-839-765-169	Sequence 169, App
31	483.5	75.3	116	3	US-09-136-389-169	Sequence 169, App
32	483.5	75.3	116	3	US-08-484-537-5	Sequence 5, Appli
33	483.5	75.3	116	3	US-09-610-838-169	Sequence 169, App
34	483.5	75.3	116	4	US-09-711-485-169	Sequence 169, App
35	483.5	75.3	116	1	US-08-303-569B-31	Sequence 31, Appl
36	483.5	75.3	116	3	US-08-474-040-19	Sequence 19, Appl
37	483.5	75.3	116	1	US-08-487-200-19	Sequence 19, Appl
38	483.5	75.3	135	1	US-08-484-537-19	Sequence 19, Appl
39	483.5	75.3	135	4	US-07-634-278-19	Sequence 19, Appl
40	483.5	75.3	135	3	US-08-477-728-19	Sequence 19, Appl
41	483.5	75.3	135	2	US-09-355-925-7	Sequence 7, Appli
42	483.5	75.3	139	4	US-09-355-925-8	Sequence 8, Appli
43	483.5	75.3	139	4	US-09-269-921-125	Sequence 125, App
44	483.5	75.3	139	4	US-09-269-921-128	Sequence 128, App
45	483	75.2	117	3	US-08-525-539A-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1
US-08-137-117D-102
Sequence 102, Application US/08137117D
Patent No. 5795965

GENERAL INFORMATION:
;   APPLICANT: TSUCHIYA, Masayuki
;   APPLICANT: SATO, Koh
;   APPLICANT: BENDIG, Mary
;   APPLICANT: JONES, Steven
;   APPLICANT: SALDANHA, Jose
;   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;   TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
;   NUMBER OF SEQUENCES: 158
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 3000 K Street, N.W., Suite 500
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/137,117D
;   FILING DATE: 20-DEC-1993
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/JP92/00544
;   FILING DATE: 24-APR-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 4-32084
;   FILING DATE: 19-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 3-95476
;   FILING DATE: 25-APR-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: WEGNER, Harold C.
;   REGISTRATION NUMBER: 25,258
;   REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)672-5300
;   TELEFAX: (202)672-5399
;   TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 102:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 135 amino acids
;   TYPE: amino acid

Query Match
US-08-137-117D-102
Best Local Similarity   77.5%;   Score 497.5; DB 1; Length 135;
Matches   94; Conservative 11; Mismatches 11; Indels   3; Gaps   1;

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Db  20  QVQLVQSGAEVKKPGASVKVSCKASGYFTSYYIHWVRQAPCQGLEWIGYIDPFNGGTSY  79

Qy  61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS  119
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Db  80  NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGN---RFAYWGQGTLVTVSS  135
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RESULT 2
US-08-436-717-102
Sequence 102, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
    APPLICANT: TSUCHIYA, Masayuki
    APPLICANT: SATO, Koh
    APPLICANT: BENDIG, Mary
    APPLICANT: JONES, Steven
    APPLICANT: SALDANHA, Jose
    TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
    TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
    NUMBER OF SEQUENCES: 158
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Foley & Lardner
        STREET: 3000 K Street, N.W., Suite 500
        CITY: Washington
        STATE: D.C.
        COUNTRY: USA
        ZIP: 20007-5109
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/436,717
        FILING DATE:
        CLASSIFICATION:
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 536
        FILING DATE: 20-DEC-1993
        APPLICATION NUMBER: US/08/137,117
        FILING DATE: 24-APR-1992
        APPLICATION NUMBER: WO PCT/JP92/00544
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: JP 4-32084
        FILING DATE: 19-FEB-1992
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: JP 3-95476
        FILING DATE: 25-APR-1991
    ATTORNEY/AGENT INFORMATION:
        NAME: WEGNER, Harold C.
        REGISTRATION NUMBER: 25,258
        REFERENCE/DOCKET NUMBER: 53466/126/AAOK
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (202)672-5300
        TELEFAX: (202)672-5399
        TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 135 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
    MOLECULE TYPE: protein

Query Match
US-08-561-521-41
Best Local Similarity   77.5%;   Score 497.5; DB 2; Length 135;
Matches   94; Conservative 11; Mismatches 11; Indels   3; Gaps   1;

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        ||||||||||||||||||||||:||:|:|||||||||||||||||:||||||:
Db  20  QVQLVQSGAEVKKPGASVKVSCKASGYFTSYYIHWVRQAPCQGLEWIGYIDPFNGGTSY  79

Qy  61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS  119
        |||||||||| |||||||||||||||||||||||||||      |||||||||||||||
Db  80  NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGN---RFAYWGQGTLVTVSS  135
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RESULT 3
US-08-561-521-41
Sequence 41, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
    APPLICANT: Bendig, Mary M.
    APPLICANT: Leger, Olivier J.
    APPLICANT: Saldanha, Jose
    APPLICANT: Jones, S. Tarran
    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
    TITLE OF INVENTION: Adhesion Molecule VLA-4
    NUMBER OF SEQUENCES: 45
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Townsend and Townsend Khourie and Crew
        STREET: One Market Plaza, Steuart Tower, Suite 2000
        CITY: San Francisco
        STATE: California
        COUNTRY: USA
        ZIP: 94105
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/561,521
        FILING DATE:
        CLASSIFICATION:
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 424
        FILING DATE: 25-JAN-1994
        APPLICATION NUMBER: US/08/186,269A
    ATTORNEY/AGENT INFORMATION:
        NAME: Smith, William L.
        REGISTRATION NUMBER: 30,223
        REFERENCE/DOCKET NUMBER: 15270-14
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 415-543-9600
        TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 116 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: protein

Query Match
Best Local Similarity   77.3%;   Score 496.5; DB 2; Length 116;
Matches   93; Conservative 12; Mismatches 11; Indels   3; Gaps   1;

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Qy   1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYMYMWVRQAPGKGLEWIGYIDPYYGDPGY  60
        ||||||||||||||||||||||:||:|:||||||||||||||||:||||||:
Db   1  QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPCQGLEWVGYIDPFNGGTSY  60

Qy  61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS  119
        |||||||||| |||||||||||||||||||||||||||      |||||||||||||||
Db  61  NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGN---RFAYWGQGTLVTVSS  116
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RESULT 4
PCT-US95-01219-41
Sequence 41, Application PCT/US9501219
; GENERAL INFORMATION:
;   APPLICANT: Bendig, Mary M.
;   APPLICANT: Leger, Olivier J.
;   APPLICANT: Saldanha, Jose
;   APPLICANT: Jones, S. Tarran
;   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
;   TITLE OF INVENTION: Adhesion Molecule VLA-4
;   NUMBER OF SEQUENCES: 45
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US95/01219
;   FILING DATE: 25-JAN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/186,269
;   FILING DATE: 25-JAN-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William L.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 15270-14
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-543-9600
;   TELEFAX: 415-543-5043
;   INFORMATION FOR SEQ ID NO: 41:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 116 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US95-01219-41

Query Match   77.3%;   Score 496.5; DB 5; Length 116;
Best Local Similarity   78.2%; Pred. No. 2.3e-40;
Matches 93; Conservative 12; Mismatches 11; Indels 3; Gaps 1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
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Db   1 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWVGYIDPFNGGTSY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
            ||||||| ||||||||||||||||||||||||||||| || ||:|||:||||||||||
Db   61 NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGN---RFAYWGQGTLVTVSS 116

RESULT 5
US-08-137-117D-100
; Sequence 100, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
;   APPLICANT: TSUCHIYA, Masayuki
;   APPLICANT: SATO, Koh
;   APPLICANT: BENDIG, Mary
;   APPLICANT: JONES, Steven
;   APPLICANT: SALDANHA, Jose
;   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;   TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
;   NUMBER OF SEQUENCES: 158
;   CORRESPONDENCE ADDRESS:

--- column break ---

;   ADDRESSEE: Foley & Lardner
;   STREET: 3000 K Street, N.W., Suite 500
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/137,117D
;   FILING DATE: 20-DEC-1993
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/JP92/00544
;   FILING DATE: 24-APR-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 4-32084
;   FILING DATE: 19-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: JP 3-95476
;   FILING DATE: 25-APR-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: WEGNER, Harold C.
;   REGISTRATION NUMBER: 25,258
;   REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)672-5300
;   TELEFAX: (202)672-5399
;   TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 100:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 135 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-137-117D-100

Query Match   76.6%;   Score 491.5; DB 1; Length 135;
Best Local Similarity   77.3%; Pred. No. 8.1e-40;
Matches 92; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
            :||||||:||||||||||||||:|:||||||| |||||||||||||||||||||:||||
Db   20 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWVGYIDPFNGGTSY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
            ||||||| ||||||||||||||||||||||||||||| || ||:|||:||||||||||
Db   80 NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTACYYCARGGN---RFAYWGQGTLVTVSS 135

RESULT 6
US-08-436-717-100
; Sequence 100, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
;   APPLICANT: TSUCHIYA, Masayuki
;   APPLICANT: SATO, Koh
;   APPLICANT: BENDIG, Mary
;   APPLICANT: JONES, Steven
;   APPLICANT: SALDANHA, Jose
;   TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;   TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
;   NUMBER OF SEQUENCES: 158
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 3000 K Street, N.W., Suite 500
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20007-5109

COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/436,717
  FILING DATE:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 536
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/137,117
  FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: WO PCT/JP92/00544
  FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 4-32084
  FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: JP 3-95476
  FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
  NAME: WEGNER, Harold C.
  REGISTRATION NUMBER: 25,258
  REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202)672-5300
  TELEFAX: (202)672-5399
  TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 135 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-436-717-100

Query Match   76.6%; Score 491.5; DB 2; Length 135;
Best Local Similarity 77.3%; Pred. No. 8.1e-40;
Matches   92; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        :||||||||||||||||||||.|||||||| || |||||||||||||||||||| ||||
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWVGYIDPFNGGTSY 79

Qy 61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
        |||||||| .|| || | ||||||||||||||||||| .|||||||||||||
Db 80 NQKFKGKVTMTVDISTNTAYMELSSLRSEDTACYYCARGGN---RFAYWGQGTLVTVSS 135

RESULT 7
US-07-634-278-57
; Sequence 57, Application US/0763278
; Patent No. 5530101
; GENERAL INFORMATION:
  APPLICANT: QUEEN, Cary L.
  APPLICANT: CO, Man Sung
  APPLICANT: SCHNEIDER, William P.
  APPLICANT: LANDOLFI, Nicholas F.
  APPLICANT: COELINGH, Kathleen L.
  APPLICANT: SELICK, Harold E.
  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
  NUMBER OF SEQUENCES: 113
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: 379 Lytton Avenue
    CITY: Palo Alto
    STATE: California
    COUNTRY: US
    ZIP: 94301
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS

  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/634,278
  FILING DATE: 19-DEC-1990
  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/590,274
  FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/310,252
  FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/290,975
  FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
  NAME: Smith, William M
  REGISTRATION NUMBER: 30,223
  REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 326-2400
  TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 57:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 116 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
US-07-634-278-57

Query Match   76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches   94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        :||||||||||||||||||||.|||||||| || |||||||||||||||||||| ||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy 61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
        |||| .||| .||||| | ||||||||||||| ||||| .| .|||||||||||||
Db 61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

RESULT 8
US-07-634-278-73
; Sequence 73, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
  APPLICANT: QUEEN, Cary L.
  APPLICANT: CO, Man Sung
  APPLICANT: SCHNEIDER, William P.
  APPLICANT: LANDOLFI, Nicholas F.
  APPLICANT: COELINGH, Kathleen L.
  APPLICANT: SELICK, Harold E.
  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
  NUMBER OF SEQUENCES: 113
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: 379 Lytton Avenue
    CITY: Palo Alto
    STATE: California
    COUNTRY: US
    ZIP: 94301
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/634,278
  FILING DATE: 19-DEC-1990
  CLASSIFICATION: 424
PRIOR APPLICATION DATA:

Left column

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-73

Query Match   Best Local Similarity   76.0%;   Score 488.5;   DB 1;   Length 116;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;   Pred. No. 1.3e-39;

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Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
       :|||||:||||||||||:||||:|||||||:|||||||||||||||||||:|||||||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy  61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYYFDYWGQGTLVTVSS 119
       :|||:||||||:|:.||:||||||||||||||||||||        |||||||||||
Db  61 NQKFKSKATITADESINTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116
```

RESULT 9
US-08-477-728-57
Sequence 57, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:

Right column

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-57

Query Match   Best Local Similarity   76.1%;   Score 488.5;   DB 1;   Length 116;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;   Pred. No. 1.3e-39;

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Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
       :|||||:||||||||||:||||:|||||||:|||||||||||||||||||:|||||||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy  61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYYFDYWGQGTLVTVSS 119
       :|||:||||||:|:.||:||||||||||||||||||||        |||||||||||
Db  61 NQKFKSKATITADESINTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116
```

RESULT 10
US-08-477-728-73
Sequence 73, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600

RESULT 11
US-08-474-040-57
; Sequence 57, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-73

Query Match   76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity   79.0%; Pred. No. 1.3e-39;
Matches   94; Conservative 10; Mismatches 12; Indels   3; Gaps   2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
            |||| |||||||||||||:||:::: |||||||||||||||:||||||||||| | ||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
            ||||:|| ||:|||:|::|||||||||||||||||||| |||:|||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

RESULT 12
US-08-474-040-73
; Sequence 73, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-728-73

Query Match   76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity   79.0%; Pred. No. 1.3e-39;
Matches   94; Conservative 10; Mismatches 12; Indels   3; Gaps   2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
            |||| |||||||||||||:||:::: |||||||||||||||:||||||||||| | ||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
            ||||:|| ||:|||:|::|||||||||||||||||||| |||:|||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

RESULT 13
US-08-487-200-57
; Sequence 57, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William M.
; APPLICANT: LANDOLFI, Nicholas P.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-57

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-73

Query Match   76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity   79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels   3; Gaps   2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
           :||||||||||||||||||||:|||||||:|||||:||||||||||||||||||||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
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Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

RESULT 14
US-08-487-200-73
; Sequence 73, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William M.
; APPLICANT: LANDOLFI, Nicholas P.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-487-200-73

Query Match   76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity   79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels   3; Gaps   2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
           :||||||||||||||||||||:|||||||:|||||:||||||||||||||||||||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
           |||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

```
Matches  94; Conservative  10; Mismatches  12; Indels  3; Gaps  2;

Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        :||||| |||.|||:.||||.|||.||.|.|||||||||||||.|||||||||||||:||
Db    1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGIIYPYNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
        :.|||.|.|||| |:|||||||||||||||||||||||||  .||||||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116
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RESULT 15
US-08-484-537-57
; Sequence 57, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Khourie and Crew
;   STREET: 379 Lytton Avenue
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: US
;   ZIP: 94301
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/484,537
;   FILING DATE:
; PRIOR APPLICATION DATA:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/634,278
;   FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/590,274
;   FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/310,252
;   FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/290,975
;   FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William M
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 326-2400
;   TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 57:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 116 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-484-537-57

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Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        :||||| |||.|||:.||||.|||.||.|.|||||||||||||.|||||||||||||:||
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Query Match   76.1%; Score 488.5; DB 3; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

RESULT (right column):

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        :.|||.|.|||| |:|||||||||||||||||||||||||  .||||||||||||||||
Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
        :.|||.|.|||| |:|||||||||||||||||||||||||  .||||||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116
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Search completed: December 29, 2004, 18:09:13
Job time : 21.5354 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 17:47:08 ; Search time 18.4646 Seconds
                                         (without alignments)
                                         384.304 Million cell updates/sec

Title: US-10-774-076-3
Perfect Score: 563
Sequence: 1 DIKMTQSPSSMYASLGERVT............CLQYDEPYTFGGGTKLEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
   1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
   2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
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   4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
   5: /cgn2_6/ptcdata/1/iaa/pCTUS_COMB.pep:*
   6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	551	97.9	355	3	US-08-875-811-41	Sequence 41, Appl
2	551	97.9	355	3	US-08-875-811-49	Sequence 49, Appl
3	551	97.9	355	3	US-08-875-811-64	Sequence 64, Appl
4	551	97.9	358	3	US-08-875-811-45	Sequence 45, Appl
5	551	97.9	358	3	US-08-875-811-51	Sequence 51, Appl
6	551	97.9	358	3	US-08-875-811-47	Sequence 47, Appl
7	551	97.9	379	3	US-08-875-811-43	Sequence 43, Appl
8	546	97.0	127	3	US-08-348-548-4	Sequence 4, Appli
9	546	97.0	127	5	PCT-US95-15716-4	Sequence 4, Appli
10	546	96.1	107	1	US-08-107-669D-26	Sequence 26, Appl
11	541	96.1	107	1	US-08-472-788A-26	Sequence 26, Appl
12	541	96.1	107	2	US-08-477-531B-26	Sequence 26, Appl
13	541	96.1	107	2	US-08-082-842A-26	Sequence 26, Appl
14	541	94.3	107	1	US-08-425-336-123	Sequence 123, App
15	531	94.3	107	1	US-08-488-113B-123	Sequence 123, App
16	531	94.3	107	2	US-08-646-360-123	Sequence 123, App
17	531	94.3	107	3	US-08-477-484B-123	Sequence 123, App
18	531	94.3	107	3	US-08-839-765-123	Sequence 123, App
19	531	94.3	107	3	US-09-136-389-123	Sequence 123, App
20	531	94.3	107	3	US-09-610-838-123	Sequence 123, App
21	531	94.3	107	4	US-09-711-485-123	Sequence 123, App
22	531	93.6	107	5	US-08-290-592E-21	Sequence 21, Appl
23	527	93.6	107	5	PCT-US95-10053-18	Sequence 18, Appl
24	527	93.6	215	2	PCT-US96-09448-21	Sequence 21, Appl
25	527	93.3	215	2	US-08-737-129A-8	Sequence 8, Appli
26	522	92.2	142	2	US-08-579-940-2	Sequence 2, Appli
27	522	92.7	142	3	US-08-838-692-4	Sequence 4, Appli
28	519.5	92.3	129	2	US-08-860-174A-5	Sequence 5, Appli
29	519.5	92.3	258	2	US-08-860-174A-13	Sequence 13, Appl
30	508	90.2	107	1	US-08-107-669D-27	Sequence 27, Appl
31	508	90.2	107	1	US-08-472-788A-27	Sequence 27, Appl
32	508	90.2	107	2	US-08-477-531B-27	Sequence 27, Appl
33	508	90.2	107	2	US-08-082-842A-27	Sequence 27, Appl
34	508	86.5	107	2	US-08-425-336-125	Sequence 125, App
35	487	86.5	107	1	US-08-488-113B-125	Sequence 125, App
36	487	86.5	107	1	US-08-477-484B-125	Sequence 125, App
37	487	86.5	107	1	US-08-107-669D-65	Sequence 65, Appl
38	487	86.5	107	2	US-08-472-788A-87	Sequence 87, Appl
39	487	86.5	107	2	US-08-477-531B-65	Sequence 65, Appl
40	487	86.5	107	2	US-08-646-360-125	Sequence 125, App
41	487	86.5	107	3	US-08-082-842A-87	Sequence 87, Appli
42	487	86.5	107	3	US-08-839-765-125	Sequence 125, App
43	487	86.5	107	3	US-09-136-389-125	Sequence 125, App
44	487	86.5	107	3	US-09-610-838-125	Sequence 125, App
45	487	86.5	107	4	US-09-711-485-125	Sequence 125, App

ALIGNMENTS

RESULT 1
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-41

Query Match   97.9%; Score 551; DB 3; Length 355;
Best Local Similarity   97.2%; Pred. No. 8.4e-46;

Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
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Db 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
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RESULT 2
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-24410OUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match   97.9%; Score 551; DB 3; Length 355;
Best Local Similarity 97.2%; Pred. No. 8.4e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
       |||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
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RESULT 3

US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-24410OUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note= "B6FB[Met-(-1)]SerrOnc"

Query Match   97.9%; Score 551; DB 3; Length 355;
Best Local Similarity 97.2%; Pred. No. 8.4e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
       |||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db 1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
       |||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
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RESULT 4
US-08-875-811-45
; Sequence 45, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis

; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-24410OUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-45

Query Match 97.9%; Score 551; DB 3; Length 358;
Best Local Similarity 97.2%; Pred. No. 8.5e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db  119 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS 178

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  179 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 225
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RESULT 5
US-08-875-811-51
; Sequence 51, Application US/0887581l
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-24410OUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-51

Query Match 97.9%; Score 551; DB 3; Length 358;
Best Local Similarity 97.2%; Pred. No. 8.5e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||| |||||||||| |:|||||||| ||||||||||||||||||
Db  119 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS 178

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  179 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 225
```

RESULT 6
US-08-875-811-47
; Sequence 47, Application US/0887581l
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-2441000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match   Best Local Similarity 97.9%; 97.2%;   Score 551; DB 3; Length 360;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
Db 121 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS 180

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
Db 181 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 227

RESULT 7
US-08-811-43
Sequence 43, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-2441000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-875-811-43

Query Match   Best Local Similarity 97.9%; 97.2%;   Score 551; DB 3; Length 379;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
Db 143 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS 202

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
Db 203 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 249

RESULT 8
US-08-348-548-4
; Sequence 4, Application US/08348548
; Patent No. 6258529
; GENERAL INFORMATION:
; APPLICANT: Berdoz, Jose
; APPLICANT: Kraehenbuhl, Jean Pierre
; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
; NUMBER OF SEQUENCES: 108
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,548
; FILING DATE: 01-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06132/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-5070
; TELEX: 200154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-348-548-4

Query Match   Best Local Similarity 97.0%; 95.3%;   Score 546; DB 3; Length 127;
Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
Db 21 DIKVTQSPSSMYASLGERVTITCKASQDINNYLNWFQQKPGKSPKTLIYRANRLLDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
Db 81 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQFDEFPYTFGGGTKLEIK 127

RESULT 9

PCT-US95-15716-4
; Sequence 4, Application PCT/US9515716
; GENERAL INFORMATION:
; APPLICANT: Berdoz, Jose
; APPLICANT: Kraehenbuhl, Jean Pierre
; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15716
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,548
; FILING DATE: 01-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06132/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-5070
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match   97.0%;   Score 546; DB 5; Length 127;
Best Local Similarity   95.3%;   Pred. No. 8.2e-46;
Matches 102; Conservative   5; Mismatches 0; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
         ||||||||||||||||:|||||||||||||:||:|||||||||||||||||||:||||
Db   21 DIKVTQSPSSMYASLGBRVTITCKASQDINNYLNWFQQKPGKSPKTLIYRANRLLDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
         ||||||||||||||||||||||||||||||||:|||||||||||||
Db   81 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQFDEFPYTFGGGTKLEIK 127

RESULT 10
US-08-107-669D-26
; Sequence 26, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-26

Query Match   96.1%;   Score 541; DB 1; Length 107;
Best Local Similarity   96.3%;   Pred. No. 2.1e-45;
Matches 103; Conservative   2; Mismatches 2; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
         ||||||||||||||||||:||||||||||:||||:||||||||||||
Db   61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 11
US-08-472-788A-26
; Sequence 26, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464

; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; TELEX:
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-788A-26

Query Match
Best Local Similarity   96.1%;   Score 541;   DB 1;   Length 107;
Matches 103;   Conservative 2;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          ||||||||||||||::|||||||||||:|||||:|||||||||||||
Db   61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 12
US-08-477-531B-26
; Sequence 26, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-26

Query Match
Best Local Similarity   96.1%;   Score 541;   DB 2;   Length 107;
Matches 103;   Conservative 2;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          ||||||||||||||::|||||||||||:|||||:|||||||||||||
Db   61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 13
US-08-082-842A-26
; Sequence 26, Application US/08082842A
; Patent No. 5869619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-082-842A-26

Query Match
Best Local Similarity   96.1%;   Score 541;   DB 2;   Length 107;
Matches 103;   Conservative 2;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107

Db   61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 14
US-08-425-336-123
; Sequence 123, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-123

Query Match   94.3%; Score 531; DB 1; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.9e-44;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
      ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFHHKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
      ||||||||||||||||||: ||||||| ||||: |  ||||||||||
Db 61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107
```

RESULT 15
US-08-488-113B-123
; Sequence 123, Application US/08488113B
; Patent No. 5744580

Db   61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107

; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-123

Query Match   94.3%; Score 531; DB 1; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.9e-44;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
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Db  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFHHKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
      ||||||||||||||||||: ||||||| ||||: |  ||||||||||
Db 61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107
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Search completed: December 29, 2004, 18:08:59
Job time : 19.4646 secs

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 29, 2004, 17:47:08 ; Search time 20.0177 Seconds
                  (without alignments)
                  384.304 Million cell updates/sec

Title: US-10-774-076-4
Perfect score: 617
Sequence: 1 EVQLQQSGAELVRSGASVKL.........YGGTITFAYWGQGTLVTVSA 116

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Issued Patents AA:*
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             4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
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             6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	523	84.8	118	3	US-08-767-128-22	Sequence 22, Appl
2	516	83.6	535	3	US-08-983-035A-38	Sequence 38, Appl
3	508	82.3	124	1	US-08-017-570-6	Sequence 6, Appli
4	508	82.3	124	1	US-08-471-426-6	Sequence 6, Appli
5	508	82.3	124	5	PCT-US94-01709-6	Sequence 6, Appli
6	507	82.2	136	4	US-09-564-329A-11	Sequence 11, Appli
7	507	82.2	136	4	US-09-963-620-11	Sequence 11, Appli
8	507	82.2	136	4	US-09-855-632-11	Sequence 11, Appl
9	507	82.2	136	3	US-09-423-439-44	Sequence 44, Appl
10	505	81.8	642	3	US-09-423-439-26	Sequence 26, Appl
11	505	81.8	666	3	US-09-423-439-51	Sequence 51, Appli
12	505	81.5	124	1	US-08-017-570-4	Sequence 4, Appli
13	503	81.5	124	1	US-08-471-426-4	Sequence 4, Appli
14	503	81.5	124	5	PCT-US94-01709-4	Sequence 4, Appli
15	502	81.4	255	2	US-09-171-945-19	Sequence 19, Appl
16	502	81.4	270	2	US-09-188-082-16	Sequence 16, Appl
17	501	81.2	553	2	US-08-661-052-16	Sequence 16, Appl
18	501	81.2	553	3	US-09-364-008-16	Sequence 16, Appl
19	501	81.2	553	3	US-09-188-082-16	Sequence 16, Appl
20	501	81.2	553	3	US-09-102-716-16	Sequence 16, Appl
21	500	81.0	136	5	PCT-US95-15716-8	Sequence 8, Appli
22	500	81.0	136	5	US-08-348-548-8	Sequence 8, Appl
23	498.5	80.8	254	2	US-08-792-824-4	Sequence 4, Appli
24	498.5	80.8	254	2	US-08-792-824-7	Sequence 7, Appli
25	498.5	80.8	254	2	US-08-792-824-10	Sequence 10, Appl
26	498.5	80.8	254	3	US-08-792-824-13	Sequence 13, Appl
27	496	80.4	124	3	US-09-672-609-1	Sequence 1, Appl
28	496	80.4	124	4	US-09-025-403A-1	Sequence 1, Appli
29	495.5	80.3	119	4	US-09-649-063-11	Sequence 11, Appl
30	495.5	80.3	248	4	US-09-649-063-23	Sequence 23, Appl
31	493.5	80.0	136	1	US-08-024-253-2	Sequence 2, Appli
32	490.5	79.5	136	1	US-08-290-592E-18	Sequence 18, Appl
33	490.5	79.5	117	5	PCT-US95-10053-15	Sequence 15, App
34	490.5	79.5	117	3	PCT-US96-09448-18	Sequence 18, Appl
35	487	78.9	120	3	US-09-171-945-11	Sequence 11, Appl
36	483.5	78.4	125	2	US-08-561-521-44	Sequence 44, Appl
37	483.5	78.4	125	5	PCT-US95-01219-44	Sequence 44, Appl
38	477.5	77.4	117	4	US-09-647-468-141	Sequence 141, App
39	477.5	77.4	117	4	US-09-647-468-155	Sequence 155, Appl
40	477	77.3	118	2	US-08-232-081B-38	Sequence 38, Appl
41	476.5	77.2	136	5	US-08-646-265A-29	Sequence 29, Appl
42	473.5	76.7	123	5	US-08-561-521-9	Sequence 9, Appli
43	473.5	76.7	123	3	PCT-US95-01219-9	Sequence 9, Appl
44	470	76.2	123	5	US-08-836-561-31	Sequence 31, Appli
45	470	76.2	137	4	US-09-434-122-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-767-128-22
Sequence 22, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
  APPLICANT: WYLIE, DWANE E.
  APPLICANT: LOPEZ, OSVALDO
  APPLICANT: MURRAY, PETER JOSEPH
  APPLICANT: GOEBEL, PETER JOSEPH
  TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
  TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
  NUMBER OF SEQUENCES: 46
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
    STREET: 3100 No. 6111079west Center, 90 South Seventh St
    CITY: Minneapolis
    STATE: MN
    COUNTRY: USA
    ZIP: 55402
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ Version 1.5
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/767,128
    FILING DATE:
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE: 04-DEC-1996
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
    CLASSIFICATION: 424
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/US96/09258
    FILING DATE: 05-JUN-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/541,373
    FILING DATE: 10-OCT-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/462,798
    FILING DATE: 05-JUN-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Carter, Charles G.
    REGISTRATION NUMBER: 35,093
    REFERENCE/DOCKET NUMBER: 8648.49USF1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 612/371-5278
    TELEFAX: 612/332-9081
    TELEX:
INFORMATION FOR SEQ ID NO: 22:

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SEQUENCE CHARACTERISTICS:
    LENGTH: 118 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    HYPOTHETICAL: NO
    ANTI-SENSE: NO
    FRAGMENT TYPE: internal
    ORIGINAL SOURCE:
US-08-767-128-22
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Query Match   84.8%; Score 523; DB 3; Length 118;
Best Local Similarity   86.4%; Pred. No. 2.8e-46;
Matches 102; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

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Qy  1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITFAYWGQGTLVTVSA 116
       |||||:|||||||||||||||||||||||||||||   ||||||||||||||||:
Db 61 DPKFQGKAITADTSSNIAYLQLSSLTSEDTAVYYCNPYGYDDAMDYWGQGTSVTVSS 118
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RESULT 2
US-08-983-035A-38
Sequence 38, Application US/0898035A
Patent No. 6326464
GENERAL INFORMATION:
    APPLICANT: CONSEILLER, EMMANUEL
    APPLICANT: BRACCO, LAURENT
    TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
        USES THEREOF
    NUMBER OF SEQUENCES: 59
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
            DUNNER, LLP
        STREET: 1300 I Street, NW
        CITY: Washington
        STATE: DC
        COUNTRY: USA
        ZIP: 20005-3315
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/983,035A
        FILING DATE: 20-Feb-1998
        CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/FR96/01111
        FILING DATE: 17-JUL-1996
        APPLICATION NUMBER: FR 95/08729
        FILING DATE: 19-JUL-1995
    ATTORNEY/AGENT INFORMATION:
        NAME: Strauss, William L.
        REGISTRATION NUMBER: 47,114
        REFERENCE/DOCKET NUMBER: 03804.0142
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 202-408-4000
        TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 535 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
        MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Query Match   83.6%; Score 516; DB 3; Length 535;
Best Local Similarity   84.7%; Pred. No. 9.1e-45;
Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;

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Db  3 QVQLQESGAELVGSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 62

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITFAYWGQGTLVTVSA 116
       ||:|||||||||||||||||||||||||||||||   ||||||||||||||||:
Db 63 APKFQGKATMTADTSSNTAYLQLSSLASEDTAVYYCNFYGDALD--YWGQGTSVTVSS 118
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RESULT 3
US-08-017-570-6
Sequence 6, Application US/08017570
Patent No. 5472693
GENERAL INFORMATION:
    APPLICANT: GOURLIE, BRIAN B
    APPLICANT: RIXON, MARK W
    APPLICANT: MEZES, PETER S
    APPLICANT: KAPLAN, DONALD A
    APPLICANT: SCHLOM, JEFFREY
    TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
    TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
    NUMBER OF SEQUENCES: 24
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Duane C. Ulmer
        STREET: P.O. Box 1967
        CITY: Midland
        STATE: MI
        COUNTRY: US
        ZIP: 48641-1967
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/017,570
        FILING DATE: 19930216
        CLASSIFICATION: 424
    ATTORNEY/AGENT INFORMATION:
        NAME: ULMER, DUANE C
        REGISTRATION NUMBER: 34,941
        REFERENCE/DOCKET NUMBER: C-38,777
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 124 amino acids
        TYPE: AMINO ACID
        TOPOLOGY: linear
        MOLECULE TYPE: protein
US-08-017-570-6

Query Match   82.3%; Score 508; DB 1; Length 124;
Best Local Similarity   81.5%; Pred. No. 1e-44;
Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

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        |||||||||||||||||||:|||||||||||||:||||||||||||||||||||||||
Db   1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy  61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTIT----FAYWGQGTLV 112
        ||:|||||||:||||||||||||||||||||||||        ||    ||||||||||
Db  61 APKFQGKATMTDTSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFFDVWGAGTTV 120

Qy 113 TVSA 116
        ||:
Db 121 TVSS 124
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RESULT 4
US-08-471-426-6
Sequence 6, Application US/08471426
Patent No. 5808033
GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-426-6

Query Match   82.3%; Score 508; DB 1; Length 124;
Best Local Similarity   81.5%; Pred. No. 1e-44;
Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
           |||||||||||||||||||:|||||||||||||:||:||||||||||||| ||||||||||
Db   1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTIT----FAYWGQGTLV 112
           ||:|||:|||| |||||||||||||||||||||||| ||||| ||||||| |||
Db   61 APKFQGKATMTDTSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFPDVWGAGTTV 120

Qy   113 TVSA 116
           |||:
Db   121 TVSS 124

RESULT 5
PCT-US94-01709-6
Sequence 6, Application PCT/US9401709
GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01709
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: 38,777-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-01709-6

Query Match   82.3%; Score 508; DB 5; Length 124;
Best Local Similarity   81.5%; Pred. No. 1e-44;
Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
           |||||||||||||||||||:|||||||||||||:||:||||||||||||| ||||||||||
Db   1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTIT----FAYWGQGTLV 112
           ||:|||:|||| |||||||||||||||||||||||| ||||| ||||||| |||
Db   61 APKFQGKATMTDTSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFPDVWGAGTTV 120

Qy   113 TVSA 116
           |||:
Db   121 TVSS 124

RESULT 6
US-09-564-329A-11
Sequence 11, Application US/0956432 9A
Patent No. 6541212
GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261

PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 136
TYPE: PRT
ORGANISM: SCID Mice
US-09-564-329A-11

Query Match 82.2%; Score 507; DB 4; Length 136;
Best Local Similarity 84.5%; Pred. No. 1.5e-44;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

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Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        |||||||||||||||||||||||||||||||||||||||::|||||||| ||||||||:
Db  14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy  61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA    116
        ||:|||:||||||| |||||||:||||||||||||||     ||||||||||||
Db  74 VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA    125
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RESULT 7
US-09-963-620-11
Sequence 11, Application US/09963620
Patent No. 6756036
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/963,620
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25

RESULT 8
US-09-855-632-11
Sequence 11, Application US/09855632
Patent No. 6790939
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/855,632
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 136
TYPE: PRT
ORGANISM: SCID Mice
US-09-855-632-11

Query Match 82.2%; Score 507; DB 4; Length 136;
Best Local Similarity 84.5%; Pred. No. 1.5e-44;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

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Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
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Db  14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy  61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA    116
        ||:|||:||||||| |||||||:||||||||||||||     ||||||||||||
Db  74 VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA    125
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RESULT 9
US-09-423-439-44
Sequence 44, Application US/09423439
Patent No. 6339070

Query Match 82.2%; Score 507; DB 4; Length 136;

GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
  BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Pillsbury Winthrop, L.L.P.
  STREET: 1100 New York Ave., N.W.
  CITY: Washington
  STATE: D.C.
  COUNTRY: U.S.A.
  ZIP: 2005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: MS Word
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/423,439
  FILING DATE: 09-No. 6339070-1999
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/GB98/01294
  FILING DATE: 05-MAY-1998
  APPLICATION NUMBER: GB 9709421.3
  FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
  LENGTH: 281 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-423-439-44

Query Match   81.8%; Score 505; DB 3;   Length 281;
Best Local Similarity 80.8%; Pred. No. 5.6e-44;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
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Db 23 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDTEY 82

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITFAYWGQGTLVTVSA 116
         ||:|:|.:|:||:|||||||||||||||||||||| |||||||||||||:|:
Db 83 APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 142

RESULT 10
US-09-423-439-26
Sequence 26, Application US/0942439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
  BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Pillsbury Winthrop, L.L.P.
  STREET: 1100 New York Ave., N.W.
  CITY: Washington
  STATE: D.C.
  COUNTRY: U.S.A.
  ZIP: 2005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: MS Word
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/423,439
  FILING DATE: 09-No. 6339070-1999

  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/GB98/01294
  FILING DATE: 05-MAY-1998
  APPLICATION NUMBER: GB 9709421.3
  FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  LENGTH: 642 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-423-439-26

Query Match   81.8%; Score 505; DB 3;   Length 642;
Best Local Similarity 80.8%; Pred. No. 1.5e-43;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
         |||||||||||||||||||||||||||||| |:|||||||||||||| ||||||||||
Db 20 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDTEY 79

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITFAYWGQGTLVTVSA 116
         ||:|:|.:|:||:|||||||||||||||||||||| |||||||||||||:|:
Db 80 APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 139

RESULT 11
US-09-423-439-51
Sequence 51, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
  BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Pillsbury Winthrop, L.L.P.
  STREET: 1100 New York Ave., N.W.
  CITY: Washington
  STATE: D.C.
  COUNTRY: U.S.A.
  ZIP: 2005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: MS Word
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/423,439
  FILING DATE: 09-No. 6339070-1999
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/GB98/01294
  FILING DATE: 05-MAY-1998
  APPLICATION NUMBER: GB 9709421.3
  FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
  LENGTH: 666 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

Query Match   81.8%; Score 505; DB 3;   Length 666;
Best Local Similarity 80.8%; Pred. No. 1.6e-43;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

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Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIAWIDPENGDTEY 79

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITFAYWGQGTLVTVSA 116
        ||||||||||||||||||||||||||||||||||:    :||||||||||||||:
Db   80 APKFPGRATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 139
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RESULT 12
US-08-017-570-4
; Sequence 4, Application US/08017570
; Patent No. 5472693
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/017,570
; FILING DATE: 19930216
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-08-017-570-4
; MOLECULE TYPE: protein

Query Match   81.5%; Score 503; DB 1; Length 124;
Best Local Similarity 80.6%; Pred. No. 3.4e-44;
Matches 100; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

```
Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIAWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTIT----FAYWGQGTLV 112
        ||||||||||||||||||||||||||||||||||:    :||||||    |||||||||
Db   61 APKFQGKATMTDTSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFFDVWGAGTTV 120

Qy  113 TVSA 116
        ||:
Db  121 AVSS 124
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RESULT 13
US-08-471-426-4
; Sequence 4, Application US/08471426
; GENERAL INFORMATION:
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: MEZES, PETER S
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,426
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/017,570
; FILING DATE: 16-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-38,777
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-471-426-4
; MOLECULE TYPE: protein

Query Match   81.5%; Score 503; DB 1; Length 124;
Best Local Similarity 80.6%; Pred. No. 3.4e-44;
Matches 100; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

```
Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYYMHWVKQRPEQGLEWIAWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTIT----FAYWGQGTLV 112
        ||||||||||||||||||||||||||||||||||:    :||||||    |||||||||
Db   61 APKFQGKATMTDTSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFFDVWGAGTTV 120

Qy  113 TVSA 116
        ||:
Db  121 AVSS 124
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RESULT 14
PCT-US94-01709-4
; Sequence 4, Application PCT/US9401709
; GENERAL INFORMATION:
; APPLICANT: THE DOW CHEMICAL COMPANY
; APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI

```
;   COUNTRY: US
;   ZIP: 48641-1967
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US94/01709
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: ULMER, DUANE C
;   REGISTRATION NUMBER: 34,941
;   REFERENCE/DOCKET NUMBER: 38,777-F
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (517) 636-8104
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 124 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US94-01709-4
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Query Match         81.5%;   Score 503;  DB 5;   Length 124;
Best Local Similarity  80.6%;   Pred. No. 3.4e-44;
Matches 100;   Conservative  4;  Mismatches  12;  Indels  8;  Gaps  2;

Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
          |||||||||||||||||||||||||||||||||||||| |:|||||||||||||||||||
Db    1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYYMHWVKQRPEQGLEWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITPAYWGQGTLVTVSA 116
          ||||||||||||||||||||||||||||||||||     ||||||:|||||||||
Db   61 APKFQGKATMTDTSSNTAYLQLSSLTSEDTAVYYCNTRGLSTMITTRWFFDVWGAGTTV 120
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```
Qy  113 TVSA 116
         ||:|
Db  121 AVSS 124
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RESULT 15
US-09-171-945-19
;   Sequence 19, Application US/09171945
;   Patent No. 6277599
;   GENERAL INFORMATION:
;   APPLICANT: Emery, Stephen
;   APPLICANT: Copley, Clive Graham
;   APPLICANT: Edge, Michael Derek
;   TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
;   TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
;   FILE REFERENCE: Monoclonal Antibody to CEA
;   CURRENT APPLICATION NUMBER: US/09/171,945
;   CURRENT FILING DATE: 1998-10-29
;   PRIOR APPLICATION NUMBER: GB9703103.3
;   PRIOR FILING DATE: 1997-02-14
;   PRIOR APPLICATION NUMBER: GB9609405.7
;   PRIOR FILING DATE: 1996-05-04
;   PRIOR APPLICATION NUMBER: PCT/GB97/01165
;   PRIOR FILING DATE: 1997-04-29
;   NUMBER OF SEQ ID NOS: 131
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 19
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-19
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Query Match          81.4%;   Score 502;  DB 3;   Length 255;
Best Local Similarity  80.0%;   Pred. No. 1e-43;
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Search completed: December 29, 2004, 18:09:10
Job time : 31.0177 secs
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Matches 96;   Conservative  8;  Mismatches  12;  Indels  4;  Gaps  1;

Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
          |||||||||||||||||||||||||||||||||||||| |:|||||||||||||||||||
Db   20 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYYMHWVKQRPEQGLEWIDPENGDTEY 79

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITPAYWGQGTLVTVSA 116
          ||||||||||||||||||||||||||||||||||     ||||||:|||||||
Db   80 APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 139
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 17:47:08 ; Search time 18.9823 Seconds
                   (without alignments)
                   384.304 Million cell updates/sec

Title: US-10-774-076-5
Perfect score: 576
Sequence: 1 QAVVTQESALTTSPGETVTL.........ALWYSNHWVFGGGTKLTVLG 110

Scoring table: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :   Issued_Patents_AA:*
                   1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
                   2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
                   3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
                   4: /cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
                   5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
                   6: /cgn2_6/ptcdata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	%	DB ID	Description
1	559	97.0	112	3	US-09-157-370-6	Sequence 6, Appli
2	559	97.0	269	2	US-08-428-257A-72	Sequence 72, Appli
3	559	97.0	269	2	US-08-491-988-3	Sequence 3, Appli
4	559	97.0	402	2	US-08-491-988-9	Sequence 9, Appli
5	559	97.0	415	2	US-08-491-988-7	Sequence 7, Appli
6	559	97.0	435	2	US-08-491-988-5	Sequence 5, Appli
7	548	95.1	128	2	US-08-348-548-2	Sequence 2, Appli
8	548	95.1	128	5	PCT-US95-15716-2	Sequence 2, Appli
9	530.5	92.1	110	4	US-09-865-483-7	Sequence 7, Appli
10	528	91.7	110	1	US-08-122-546-14	Sequence 14, Appl
11	528	91.7	110	2	US-08-764-938-14	Sequence 14, Appl
12	528	91.7	110	3	US-09-131-052-14	Sequence 14, Appl
13	528	91.7	110	3	US-09-131-053A-14	Sequence 14, Appl
14	520	90.3	106	2	US-08-440-354-2	Sequence 2, Appli
15	520	90.3	106	2	US-08-463-087-2	Sequence 2, Appli
16	517	89.8	109	2	US-08-672-345C-1	Sequence 1, Appli
17	517	89.8	109	2	US-09-214-095D-1	Sequence 1, Appli
18	513	89.1	109	2	US-08-672-345C-2	Sequence 2, Appli
19	513	89.1	109	2	US-09-214-095D-2	Sequence 2, Appli
20	509	88.4	115	6	5215889-3	Patent No. 5215889
21	504	87.5	109	2	US-08-672-345C-3	Sequence 3, Appli
22	504	87.5	109	3	US-09-214-095D-3	Sequence 3, Appli
23	504	87.5	109	3	US-09-214-095D-121	Sequence 121, App
24	502	87.2	109	2	US-08-672-345C-93	Sequence 93, Appli
25	476	82.6	109	2	US-08-672-345C-4	Sequence 4, Appli
26	473	82.1	99	2	US-08-672-345C-91	Sequence 91, Appli
27	473	82.1	99	3	US-09-214-095D-92	Sequence 92, Appli
28	469	81.4	99	3	US-09-214-095D-88	Sequence 88, Appl
29	462	80.2	200	6	5189147-10	Patent No. 5189147
30	450.5	78.2	99	2	US-08-672-345C-92	Sequence 92, Appl
31	428	74.3	100	3	US-09-214-095D-96	Sequence 96, Appl
32	426	74.0	98	2	US-08-672-345C-94	Sequence 94, Appli
33	413.5	71.8	98	3	US-09-214-095D-4	Sequence 4, Appli
34	343.5	59.6	73	4	US-09-050-861B-5	Sequence 5, Appli
35	329	57.1	64	2	US-08-765-179B-23	Sequence 23, Appl
36	329	57.1	108	3	US-09-240-274-51	Sequence 51, Appl
37	329	57.1	108	3	US-09-240-274-52	Sequence 52, Appl
38	329	57.1	108	5	US-09-240-274-166	Sequence 166, Appl
39	316.5	54.9	240	2	US-09-049-672A-11	Sequence 11, Appl
40	315	54.7	108	3	US-09-240-274-53	Sequence 53, Appl
41	309	53.6	216	4	US-09-291-299A-8	Sequence 8, Appli
42	300	52.1	84	4	US-09-135-238B-5	Sequence 5, Appli
43	277	48.1	216	4	US-09-291-299A-10	Sequence 10, Appl
44	265.5	46.1	217	4	US-09-291-299A-7	Sequence 7, Appli
45	252	43.8	112	2	US-08-665-202-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-157-370-6

; Sequence 6, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.

US-09-157-370-6

Query Match   97.0%; Score 559; DB 3; Length 112;
Best Local Similarity 97.3%; Pred. No. 1.3e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
             |||||||||||||||||||||||||||||| |||||||||||||||| ||| |||||||
Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110

RESULT 2
US-08-428-257A-72

; Sequence 72, Application US/0842857A
; Patent No. 5885808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; APPLICANT: Epenetos, A.A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue

```
;       CITY: New York
;       STATE: NY
;       COUNTRY: USA
;       ZIP: 10016-2391
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/428,257A
;       FILING DATE: 07/05/95
;       CLASSIFICATION: 514
;   INFORMATION FOR SEQ ID NO: 72:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 269 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-428-257A-72

Query Match        97.0%;   Score 559;   DB 2;   Length 269;
Best Local Similarity  97.3%;   Pred. No. 3.6e-48;
Matches 107;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
        ||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||
Db 158  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 217

Qy  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 218  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 267


RESULT 3
US-08-491-988-3
; Sequence 3, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
;   APPLICANT: EPENETOS, AGAMEMNON A.
;   APPLICANT: SPOONER, ROBERT A.
;   APPLICANT: DEONARAIN, MAHENDRA
;   TITLE OF INVENTION: Compounds for targeting
;   NUMBER OF SEQUENCES: 29
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: McAULAY NISSEN GOLDBERG KIEL & HAND, LLP
;       STREET: 261 MADISON AVENUE
;       CITY: NEW YORK
;       STATE: NY
;       COUNTRY: USA
;       ZIP: 10016-2391
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/491,988
;       FILING DATE: 18-DEC-1995
;       CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;       NAME: GOLDBERG, JULES E.
;       REGISTRATION NUMBER: 24,408
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 212-986-4090
;       TELEFAX: 212-818-9479
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 269 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-491-988-3


Query Match        97.0%;   Score 559;   DB 2;   Length 269;
Best Local Similarity  97.3%;   Pred. No. 3.6e-48;
Matches 107;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
        ||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||
Db 158  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 217

Qy  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 218  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 267


RESULT 4
US-08-491-988-9
; Sequence 9, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
;   APPLICANT: EPENETOS, AGAMEMNON A.
;   APPLICANT: SPOONER, ROBERT A.
;   APPLICANT: DEONARAIN, MAHENDRA
;   TITLE OF INVENTION: Compounds for targeting
;   NUMBER OF SEQUENCES: 29
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: McAULAY NISSEN GOLDBERG KIEL & HAND, LLP
;       STREET: 261 MADISON AVENUE
;       CITY: NEW YORK
;       STATE: NY
;       COUNTRY: USA
;       ZIP: 10016-2391
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/491,988
;       FILING DATE: 18-DEC-1995
;       CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;       NAME: GOLDBERG, JULES E.
;       REGISTRATION NUMBER: 24,408
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 212-986-4090
;       TELEFAX: 212-818-9479
;   INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 402 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-491-988-9


Query Match        97.0%;   Score 559;   DB 2;   Length 402;
Best Local Similarity  97.3%;   Pred. No. 5.7e-48;
Matches 107;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
        ||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||
Db 158  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 217

Qy  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
        |||||||||||||||||||||||||||||||||||||||||||||||||
Db 218  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 267


RESULT 5
US-08-491-988-7
; Sequence 7, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
;   APPLICANT: EPENETOS, AGAMEMNON A.
```

APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-7

Query Match   97.0%; Score 559; DB 2; Length 415;
Best Local Similarity   97.3%; Pred. No. 5.9e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||||| |||||||||||||||||| ||| |||
Db 158 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 217

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 218 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 267

RESULT 6
US-08-491-988-5
Sequence 5, Application US/0849198 8
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-5

Query Match   97.0%; Score 559; DB 2; Length 435;
Best Local Similarity   97.3%; Pred. No. 6.3e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||||| |||||||||||||||||| ||| |||
Db 158 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 217

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db 218 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 267

RESULT 7
US-08-348-548-2
Sequence 2, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-548-2

Query Match   95.1%; Score 548; DB 3; Length 128;
Best Local Similarity   96.3%; Pred. No. 1.9e-47;
Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 8
PCT-US95-15716-2
Sequence 2, Application PCT/US9515716
```
; GENERAL INFORMATION:
; APPLICANT: Berdoz, Jose
; APPLICANT: Kraehenbuhl, Jean Pierre
; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
; NUMBER OF SEQUENCES: 108
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: PCT/US95/15716
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,548
; FILING DATE: 01-DEC-1994
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06132/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-5070
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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PCT-US95-15716-2

```
Query Match             95.1%;  Score 548;  DB 5;  Length 128;
Best Local Similarity   96.3%;  Pred. No. 1.9e-47;
Matches  105;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 79

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 128
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RESULT 9
US-09-865-483-7
Sequence 7, Application US/09865483
```
; Patent No. 6680053
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SU
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/09/865,483
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
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US-09-865-483-7

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Query Match             92.1%;  Score 530.5;  DB 4;  Length 109;
Best Local Similarity   93.6%;  Pred. No. 8.9e-46;
Matches  103;  Conservative   3;  Mismatches   3;  Indels   1;  Gaps   1;

Qy    1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          ||||||||||||||||||||||||||| ||.:.|||||||||||||||||||| |||
Db    1 QAVVTQESALTTSPGETVTLTCRSSTGAITTNPANWVQEKPDHLFTGLIGGTINRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||||||||||||||||||||||||||||   |||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWY-NNWVFGGGTKLTVLG 109
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RESULT 10
US-08-122-546-14
Sequence 14, Application US/08122546
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; Patent No. 559159
; GENERAL INFORMATION:
; APPLICANT: Courtenay-Luck, Nigel S
; TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
; TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E Goldberg, Esq.
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/122,546
; FILING DATE: 09/29/93
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24,408
; REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 986-4090
; TELEFAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-122-546-14

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Query Match             91.7%;  Score 528;  DB 1;  Length 110;
Best Local Similarity   91.8%;  Pred. No. 1.6e-45;
Matches  101;  Conservative   2;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLLTGLIGGTINRVPGV 60
          |||:||| ||||||||||||||||||||||||||:|||||||||||||||||| |||
Db    1 QAVLTQEFALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLLTGLIGGTINRAPGV 60
```

```
Qy        61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
             |||||||||||||||||||||||||||||||||||||||||||||:||
Db        61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLSRLG 110
```

```
RESULT 11
US-08-764-938-14
; Sequence 14, Application US/0876938
; Patent No. 583943
; GENERAL INFORMATION:
;   APPLICANT: Courtenay-Luck, Nigel S
;   TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
;   TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Jules E Goldberg, Esq.
;     STREET: 261 Madison Avenue
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10016
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/764,938
;     FILING DATE: December 13, 1996
;     CLASSIFICATION: 536
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Goldberg, Jules E
;     REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT/C
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 986-4090
;     TELEFAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 110 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-764-938-14

Query Match         91.7%;  Score 528;  DB 2;  Length 110;
Best Local Similarity   91.8%;  Pred. No. 1.6e-45;
Matches 101;  Conservative   2;  Mismatches   7;  Indels   0;  Gaps   0;

Qy         1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
             |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 QAVLTQEFALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLLTGLIGGTNNRAPGV 60

Qy        61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
             |||||||||||||||||||||||||||||||||||||||||||||:||
Db        61 PARFSGSLIGDKAALTITGAQTEDEATYFCALWYSNHWVFGGGTKLSRLG 110
```

```
RESULT 12
US-09-131-052-14
; Sequence 14, Application US/09131052
; Patent No. 6107469
; GENERAL INFORMATION:
;   APPLICANT: Courtenay-Luck, Nigel S
;   TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
;   TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Jules E Goldberg, Esq.
;     STREET: 261 Madison Avenue
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10016-2391
```

```
COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/131,052
;     FILING DATE: August 7, 1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Goldberg, Jules E
;     REFERENCE/DOCKET NUMBER: JG-EPC-1069C-3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 986-4090
;     TELEFAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 110 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-131-052-14

Query Match         91.7%;  Score 528;  DB 3;  Length 110;
Best Local Similarity   91.8%;  Pred. No. 1.6e-45;
Matches 101;  Conservative   2;  Mismatches   7;  Indels   0;  Gaps   0;

Qy         1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
             |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 QAVLTQEFALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLLTGLIGGTNNRAPGV 60

Qy        61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
             |||||||||||||||||||||||||||||||||||||||||||||:||
Db        61 PARFSGSLIGDKAALTITGAQTEDEATYFCALWYSNHWVFGGGTKLSRLG 110
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RESULT 13
US-09-131-053A-14
; Sequence 14, Application US/09131053A
; Patent No. 6174691
; GENERAL INFORMATION:
;   APPLICANT: Courtenay-Luck, Nigel S
;   TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
;   TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
;   NUMBER OF SEQUENCES: 18
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Jules E Goldberg, Esq.
;     STREET: 261 Madison Avenue
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10016-2391
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/131,053A
;     FILING DATE: August 7, 1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Goldberg, Jules E
;     REFERENCE/DOCKET NUMBER: JG-EPC-1069C-2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 986-4090
;     TELEFAX: (212) 818-9479
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 110 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
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US-09-131-053A-14

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Qy  Query Match          91.7%;   Score 528;   DB 3;   Length 110;
Db  Best Local Similarity  91.8%;   Pred. No. 1.6e-45;
    Matches 101;   Conservative 2;   Mismatches 7;   Indels 0;   Gaps 0;

Qy      1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
            ||:|||||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 QAVLTQEPALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLLTGLIGGTNNRAPGV 60

Qy     61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
            |||||||||||||||||||||||||||||||:||||||   | :  | ||
Db     61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLSRIG 110
```

RESULT 14
US-08-440-354-2
; Sequence 2, Application US/08440354
; Patent No. 5907034
; GENERAL INFORMATION:
;   APPLICANT: Boblet, Klaus
;   APPLICANT: Hermentin, Peter
;   APPLICANT: Seemann, Gerhard
;   TITLE OF INVENTION: A Monoclonal Antibody Against Complexed
;   TITLE OF INVENTION: and No. 5907034Complexed Complexing Agents for Removing Heavy
;   TITLE OF INVENTION: Metals from Aqueous Solutions and for Analysis
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;   ADDRESSEE: Dunner
;   STREET: 1300 I Street, N.W.
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 2005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/440,354
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   CLASSIFICATION:
;   APPLICATION NUMBER: US/08/013,166
;   FILING DATE: 02-FEB-1993
;   APPLICATION NUMBER: US/07/664,789
;   FILING DATE: 05-MAR-1991
;   APPLICATION NUMBER: DE 4007079.4
;   FILING DATE: 07-MAR-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lavin Jr., Lawrence M.
;   REGISTRATION NUMBER: 30,768
;   REFERENCE/DOCKET NUMBER: HOAG-1043
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 408-4000
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-440-354-2

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Qy  Query Match          90.3%;   Score 520;   DB 2;   Length 106;
Db  Best Local Similarity  93.3%;   Pred. No. 9.6e-45;
    Matches 98;   Conservative 2;   Mismatches 5;   Indels 0;   Gaps 0;

Qy      4 VTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVPAR 63
            :||||||||||||||||||||||||||||||    | |||||  ||||||| || |||||
Db      2 LTQESALTTSPGETVTLTCRSSTGAVTTSNYATWVQEKPDHLLTGLIGGTKNRAPGVPAR 61
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US-09-131-053A-14

```
Qy     64 FSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTV 108
            ||||||||||||||||||||||||||||||||||||||| :
Db     62 FSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLKI 106
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RESULT 15
US-08-463-087-2
; Sequence 2, Application US/08463087
; Patent No. 5908790
; GENERAL INFORMATION:
;   APPLICANT: Boblet, Klaus
;   APPLICANT: Hermentin, Peter
;   APPLICANT: Seemann, Gerhard
;   TITLE OF INVENTION: A Monoclonal Antibody Against Complexed
;   TITLE OF INVENTION: and No. 5908790Complexed Complexing Agents for Removing Heavy
;   TITLE OF INVENTION: Metals from Aqueous Solutions and for Analysis
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;   ADDRESSEE: Dunner
;   STREET: 1300 I Street, N.W.
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/463,087
;   FILING DATE:
;   PRIOR APPLICATION DATA:
;   CLASSIFICATION: 435
;   APPLICATION NUMBER: US/07/664,789
;   FILING DATE: 05-MAR-1991
;   APPLICATION NUMBER: DE 4007079.4
;   FILING DATE: 07-MAR-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Lavin Jr., Lawrence M.
;   REGISTRATION NUMBER: 30,768
;   REFERENCE/DOCKET NUMBER: HOAG-1043
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 408-4000
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 106 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-463-087-2

```
Qy  Query Match          90.3%;   Score 520;   DB 2;   Length 106;
Db  Best Local Similarity  93.3%;   Pred. No. 9.6e-45;
    Matches 98;   Conservative 2;   Mismatches 5;   Indels 0;   Gaps 0;

Qy      4 VTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVPAR 63
            :||||||||||||||||||||||||||||||    | |||||  ||||||| || |||||
Db      2 LTQESALTTSPGETVTLTCRSSTGAVTTSNYATWVQEKPDHLLTGLIGGTKNRAPGVPAR 61

Qy     64 FSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTV 108
            ||||||||||||||||||||||||||||||||||||||| :
Db     62 FSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLKI 106
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Search completed: December 29, 2004, 18:09:12
Job time : 20.9823 secs

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                    GenCore version 5.1.6

          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        December 29, 2004, 17:46:45 ; Search time 14,677 Seconds
                                              (without alignments)
                                              701.451 Million cell updates/sec

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Title:       US-10-774-076-14
Perfect score: 561
Sequence:    1 DIQMTQSPSSLSASVGDRVT.........CLQYDEFPYTFGGGTKVEIK 107

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:    283416 seqs, 96216763 residues

Database :    PIR_79:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:      283416

                                SUMMARIES
Result                %
No.  Score  Query  Match Length DB  ID       Description
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  1  486    86.6   127   2   S52447    Ig kappa chain V r
  2  474    84.5   128   1   KVMST1    Ig kappa chain pre
  3  470    83.8   234   2   S14237    Ig kappa chain pre
  4  459    81.8   128   2   PL0101    Ig kappa chain pre
  5  453    80.7   129   2   S52789    Ig kappa chain V r
  6  452    80.6   125   2   S40333    Ig kappa chain V-J
  7  451    80.4   107   2   S36264    Ig lambda chain V
  8  451    80.4   108   2   B49047    Ig kappa chain V r
  9  450    80.2   132   2   S40334    Ig kappa chain - h
 10  449    80.0   129   2   S40369    Ig kappa chain V-J
 11  447    79.7   123   2   S40313    Ig kappa chain V r
 12  446    79.5   106   2   S20652    Ig kappa chain V r
 13  444    79.1   108   1   KIHUAU    Ig kappa chain V-I
 14  444    79.1   125   2   I39154    Ig kappa chain (BR
 15  444    79.1   125   2   S40349    Ig kappa chain V-J
 16  443    79.0   108   1   KIHUBN    Ig kappa chain V-I
 17  442    78.8   108   1   KIHURY    Ig kappa chain V-I
 18  442    78.8   115   2   KVMSL6    Ig kappa chain pre
 19  442    78.8   123   2   S40331    Ig kappa chain V-J
 20  441    78.6   108   1   KIHUWE    Ig kappa chain V-I
 21  440    78.4   108   1   S19674    Ig kappa chain V-I
 22  440    78.4   125   2   S40316    Ig kappa chain - h
 23  439    78.3   107   2   I69017    Ig kappa chain - h
 24  439    78.3   108   1   KIHURE    Ig kappa chain V-I
 25  439    78.3   125   2   S40353    Ig kappa chain V-J
 26  439    78.3   127   2   S40367    Ig kappa chain V-J
 27  438    78.1   125   2   S40350    Ig kappa chain V-J
 28  436    77.7   104   2   S13700    Ig kappa chain v r
 29  436    77.7   117   2   S46371    Ig kappa chain V-J
 30  436    77.7   129   2   S40317    Ig kappa chain - h
 31  436    77.7   129   2   S52793    Ig kappa chain V r
 32  435    77.5   117   2   S46376    Ig kappa chain V-J
 33  434    77.4   110   2   S44118    Ig kappa chain - h
 34  434    77.4   107   2   S36269    Ig lambda chain V
 35  432    77.0   108   1   KIHUHU    Ig kappa chain V-I
 36  432    77.0   141   2   A49134    Ig kappa chain V-I
 37  430    76.6   98    2   PH1065    Ig kappa chain V-I
 38  428    76.3   109   2   S31998    Ig kappa chain - h
 39  427    76.3   131   2   S40352    Ig kappa chain V-J
 40  427.5  76.2   131   2   KIHUAR    Ig kappa chain V-I
 41  427    76.1   108   1   KIHUGL    Ig kappa chain V-I
 42  427    76.1   108   1   KIHUGI    Ig kappa chain V-I
 43  427    76.1   108   1   KIHULY    Ig kappa chain V-I
 44  426.5  76.0   124   2   S40336    Ig kappa chain V-J
 45  426    75.9   108   1   KIHUKU    Ig kappa chain V-I
```

                                ALIGNMENTS

RESULT 1
S52447
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
A;Accession: S52447
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged ge
A;Residues: 1-127 <BER>
A;Cross-references: EMBL:X82688; NID:g673443; PIDN:CAA58009.1; PID:g673444
C;Genetics:
A;Reference number: S52445
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match   86.6%; Score 486; DB 2; Length 127;
Best Local Similarity 83.2%; Pred. No. 7.1e-35;
Matches 89; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
          ||::|||:|||.|::|.||||||||||||||:||.||:||||||||||||||:|||||||
Db   21 DIKVTQSPSSMYASLGERVTITCKASQDINNYLNWFQQKPGKSPKTLIYRANRLLDGVPS 80

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   81 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQFDEFPYTFGGGTKLEIK 127

RESULT 2
KVMST1
Ig kappa chain precursor V region (T1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1980 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
C;Accession: A01920
R;Altenburger, W.; Steinmetz, M.; Zachau, H.G.
Nature 287, 603-607, 1980
A;Title: Functional and non-functional joining in immunoglobulin light chain genes of a
A;Reference number: A01920; MUID:81052342; PMID:6776411
A;Accession: A01920
A;Molecule type: mRNA
A;Residues: 1-128 <ALT>
A;Cross-references: UNIPROT:P01637; GB:V00772; NID:g51636; PIDN:CAA24150.1; PID:g762979
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Introns: 17/1
C;Genetics:
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer;
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-128/Product: Ig kappa chain V region (T1) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
F;43-108/Disulfide bonds: #status predicted

Query Match   84.5%;   Score 474; DB 1; Length 128;
Best Local Similarity   81.3%;   Pred. No. 7.6e-34;
Matches   87; Conservative   13; Mismatches   7; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||||:|:||||||||||:|||||||||||||||||||||||| |||||||||
Db   21 DIKMTQSPSSMYASLGERVTISCKASQDINSYLTWFQQKPGKSPKTLIYRANRLVDGVPS 80

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||||:|:|||||:|||||||||||||||||||||:|:|
Db   81 RFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGAGTKLELK 127

RESULT 3
S14237
Ig kappa chain precursor (15C5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S14237
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibody d
A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Accession: S14237
A;Molecule type: mRNA
A;Residues: 1-234 <VAN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match   83.8%;   Score 470; DB 2; Length 234;
Best Local Similarity   81.3%;   Pred. No. 3e-33;
Matches   87; Conservative   11; Mismatches   9; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||:|:||||||||||:|||||||||||||||||||||||| |||||||||
Db   21 DIKMTQSPSSMYASLGERVTVISCKASQDINSYLSWIQQKPGKSPKTLIYRGNRLVAGVPS 80

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||||:|:|||||:|||||||||||||:||||:|:|:|
Db   81 RFSGSGSGQDYSLTISSLEYEDVGVYYCLRVDEFPFTFGSGTKLEIK 127

RESULT 4
P1Q101
Ig kappa chain precursor V region (40-140) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: P1Q101
R;Near, R.I.; Haber, E.
Mol. Immunol. 26, 371-382, 1989
A;Title: Characterization of the heavy and light chain immunoglobulin variable region ge
A;Reference number: P1Q100; MUID:89238344; PMID:2497340
A;Accession: P1Q101
A;Molecule type: DNA
A;Residues: 1-128 <NEA>
A;Experimental source: strain A/J
A;Note: the VK40-140 gene segment can be classified as a member of the Vk9 subgroup
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-114/Domain: V segment #status predicted <VRB>

F;36-110/Domain: immunoglobulin homology <IMM>
F;115-128/Domain: J segment #status predicted <JRE>

Query Match   81.8%;   Score 459; DB 2; Length 128;
Best Local Similarity   80.4%;   Pred. No. 1.5e-32;
Matches   86; Conservative   11; Mismatches   10; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||:|:||||||||||:||||||||||||||||||||| |||||:|||||||
Db   21 DIKMTQSPSSMYASLGERVTITCKASQDINSYLTWFQQKPGKSPKTLIYRTKRLVDGVPS 80

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||||:|:|||||:|||||||||||||||||:|:|:|:|
Db   81 RFSGSGSGQEYSLTISSLEYEDMGIYFCLQYDEFLLTFGAGTKLELK 127

RESULT 5
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   80.7%;   Score 453; DB 2; Length 129;
Best Local Similarity   80.4%;   Pred. No. 4.8e-32;
Matches   86; Conservative   9; Mismatches   12; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||:|:|||||||||:|||||||:|||||||||||||:|||||||||||||
Db   23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYAASSLETGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||||:|:|||||:|||||||||||||:||||:|:|:|
Db   83 RFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGGGTKVEIK 129

RESULT 6
S40333
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40333
A;status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match   80.6%;   Score 452; DB 2; Length 125;
Best Local Similarity   78.5%;   Pred. No. 5.7e-32;
Matches   84; Conservative   14; Mismatches   9; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         |||||||||||||||||||||||||||||||||||||||||||

RESULT 7
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36264
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36264
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Superfamily: immunoglobulin V region; immunoglobulin
A;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   80.4%;   Score 451;   DB 2;   Length 107;
Best Local Similarity   79.4%;   Pred. No. 6e-32;
Matches   85;   Conservative   10;   Mismatches   12;   Indels   0;   Gaps   0;

Qy   1 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS 60
            :|||||||| ||||||||||||||||:|| | |||||||||||||||| ||||| :||
Db   1 EIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            ||||||| |||||||||||||||||||||| | || |||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPVTFGQGTKVDIK 107

RESULT 8
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin
F;16-90/Domain: immunoglobulin homology

Query Match   80.4%;   Score 451;   DB 2;   Length 108;
Best Local Similarity   82.2%;   Pred. No. 6e-32;
Matches   88;   Conservative   6;   Mismatches   13;   Indels   0;   Gaps   0;

Qy   1 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS 60
            :|||||||| ||||||||||||||||:|| | |||||||||||||||| ||||| :||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            |||||||| |||||||||||||||||||| | || |||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSYSTPLTFGGGTKVEIK 107

RESULT 9

Db   19 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS 78

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            |||||||| |||||||||||||||||||| | || |||||||||
Db   79 RFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYPVTFGQGTKVEIK 125

S40334
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
A;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match   80.2%;   Score 450;   DB 2;   Length 132;
Best Local Similarity   77.6%;   Pred. No. 8.8e-32;
Matches   83;   Conservative   14;   Mismatches   10;   Indels   0;   Gaps   0;

Qy   1 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS 60
            :||||:|| |||||||||||||||||||:|| | | ||||||||||||||:| | :||
Db   22 DIQLTQSPSFLSASIGDRVTITCRASQGINSYLAWYQQKPGKAPKLLIYVASTLQSGVPS 81

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            |||||||| |||||||||||||||||||| | || |||||||||
Db   82 RFSGSGSGTEFTLTISSLQPEDFASYYCQQYNSYPVTFGGGTKVEIR 128

RESULT 10
S40369
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40369
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40369
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
A;Superfamily: immunoglobulin V region; immunoglobulin homology
A;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match   80.0%;   Score 449;   DB 2;   Length 129;
Best Local Similarity   79.4%;   Pred. No. 1.1e-31;
Matches   85;   Conservative   11;   Mismatches   11;   Indels   0;   Gaps   0;

Qy   1 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS 60
            :|||||||| |||||||||||||||||||:|| | | ||||||||||||||:| | :||
Db   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
            |||||||| |||||||||||||||||||| | || |||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSYPLTFGGGTKLEIK 107

RESULT 11
S40313
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40313
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40313
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PID:g441315
C;Superfamily: immunoglobulin V region; immunoglobulin; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match   79.7%; Score 447; DB 2; Length 123;
Best Local Similarity   81.3%; Pred. No. 1.5e-31;
Matches   87; Conservative   8; Mismatches   12; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||||||||||||||| :|:|||| ||||||||||||| :|||||||
Db   17 DIQTQSPSSLSASVGDRVTITCRASQGIRNDLAWFQQKPGKAPKRLIYDAASLLSGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLCQYDEFPYTFGGGTKVEIK 107
         |||||||| |:||||||||||||||||| |:||
Db   77 RFSGSGSGTEFTLTISSLQPEDFATYYCLCQYNGYPRTFGCGTKVEIK 123

RESULT 12
S20652
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S20652
R;Losman, M.; Fahy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Molecule type: DNA
A;Status: preliminary
A;Accession: S20652
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264

Query Match   79.5%; Score 446; DB 2; Length 106;
Best Local Similarity   77.4%; Pred. No. 1.6e-31;
Matches   82; Conservative   15; Mismatches   9; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||:||||||: ||:|.|||||||||||||||.||||||| .|||.|||| :.:|||:.||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLNWFQQKPGSRPRTLIYSRSNRLVHGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEI 106
         |||||||| |.: |:|||| : |:.|:||||||||||:|||||:||
Db   61 RFSGSGSGLYFSLSISSLEYEDMGIYYCLQYDDFPYTFGSGTKLEI 106

RESULT 13
KIHUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01594
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:77022433; PMID:1234024

A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods
FEBS Lett. 222, 6-10, 1987
R;Steiner, V.; Chang, J.Y.
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances th
C;Accession: S02572
A;Reference number: S02572; MUID:88005152; PMID:3115831
C;Keywords: heterotetramer; immunoglobulin
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
A;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match   79.1%; Score 444; DB 1; Length 108;
Best Local Similarity   79.4%; Pred. No. 2.4e-31;
Matches   85; Conservative   7; Mismatches   15; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         |||||||||||||||||||||| :||||||.|| :||||||||||| |||| |.||||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASLESGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLCQYDEFPYTFGGGTKVEIK 107
         |||||||| | |:||||||| ||||| ||:| |.|||.||||||
Db   61 RFSGSGSGAHFTFISSLQPEDIATYYCQQYDVLPWIFGQGTKVEIK 107

RESULT 14
I39154
Ig kappa chain (BRB) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: I39154
R;Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A propose
A;Reference number: I39154; MUID:96003804; PMID:7568160
A;Accession: I39154
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-108 <RES>
A;Cross-references: EMBL:U31344; NID:g944925; PIDN:AAA79238.1; PID:g944926
C;Superfamily: immunoglobulin V region; immunoglobulin; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   79.1%; Score 444; DB 2; Length 108;
Best Local Similarity   80.4%; Pred. No. 2.4e-31;
Matches   86; Conservative   6; Mismatches   15; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         |||||||||||||||||||||| :||||||.| :||||||||| |||| |.||.||||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLIWYQQKPGKAPNLLIYDASTLETGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLCQYDEFPYTFGGGTKVEIK 107
         |||||||| | |:||||||| ||||| ||:| |.||||||||||
Db   61 RFSGSGSGTEYTFTISSLQPEDIATYYCQQYDDLPYTFGGGTKVEIK 107

RESULT 15
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match   79.1%; Score 444; DB 2; Length 125;
Best Local Similarity   80.2%; Pred. No. 2.7e-31;
Matches   85; Conservative   10; Mismatches   11; Indels   0; Gaps   0;

Qy   2 IQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPSR 61
               | :|||||||||||||| |||:| ||| ||: || | :|| || |||| | | ||||
Db   19 IQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKRAPKLLIYDASSLESGVPSR 78

Qy   62 FSGSGSGQDYTLTISSLQPEDFATYYCLQYDBFPYTFGGGTKVEIK 107
               |:||||||| |||||||||||||||||| | :| ||||||||||||
Db   79 FSGSGSGTDFTLTISSLQPEDFATYYCQQRNTYPLTFGGGTKVEIK 124

Search completed: December 29, 2004, 18:06:58
Job time : 14.8437 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 18:05:34

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Title:          US-10-774-076-14
Perfect Score:  561
Sequence:       1 DIQMTQSPSSLSASVGDRVT.........CLQYDEFPYTFGGGTKVEIK 107
Scoring table:  GapOp 10.0 , GapExt 0.5
Searched:       1599051 seqs, 359727711 residues
Database :      BLOSUM62
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Total number of hits satisfying chosen parameters: 1599051

Post-processing: Minimum Match 100%
                 Listing first 45 summaries

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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; Search time 61.8643 Seconds
; (without alignments)
; 622.182 Million cell updates/sec

Database :
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 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Published_Applications AA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	561	100.0	107	17	US-10-774-076-14	Sequence 14, Appl
2	561	100.0	127	17	US-10-774-076-19	Sequence 19, Appl
3	510	90.9	107	9	US-09-158-120A-20	Sequence 20, Appl
4	503	89.7	107	17	US-10-774-076-3	Sequence 3, Appli
5	503	89.7	127	17	US-10-774-076-11	Sequence 11, Appl
6	502	89.5	107	14	US-10-340-189-27	Sequence 27, Appl
7	502	89.5	107	15	US-10-325-696-27	Sequence 27, Appl
8	499	88.9	107	16	US-10-462-062-107	Sequence 107, Appl
9	499	88.9	107	15	US-10-472-905A-96	Sequence 96, Appl
10	499	88.9	127	15	US-10-462-062-182	Sequence 182, App
11	499	88.9	127	16	US-10-472-905A-122	Sequence 122, App
12	498	88.8	107	14	US-10-127-890-125	Sequence 125, App
13	498	88.8	107	14	US-10-340-189-87	Sequence 87, Appl
14	498	88.8	107	15	US-10-325-696-65	Sequence 65, Appl
15	498	88.8	107	15	US-10-436-782-33	Sequence 33, Appl
16	496	88.4	107	15	US-10-436-783-1	Sequence 1, Appli
17	495	88.2	240	14	US-10-127-890-147	Sequence 147, App
18	495	88.2	240	14	US-10-127-890-148	Sequence 148, App
19	493	87.9	107	15	US-10-462-062-99	Sequence 99, Appl
20	493	87.9	107	15	US-10-472-905A-88	Sequence 88, Appl
21	493	87.9	107	16	US-10-462-062-180	Sequence 180, App
22	493	87.9	127	16	US-10-472-905A-120	Sequence 120, App
23	491	87.5	107	15	US-10-412-406-8	Sequence 8, Appli
24	491	87.5	663	15	US-10-412-406-32	Sequence 32, Appl
25	491	87.5	4852	15	US-10-412-406-33	Sequence 33, Appl
26	489	87.2	107	15	US-10-462-062-93	Sequence 93, Appl
27	489	87.2	107	15	US-10-472-905A-82	Sequence 82, Appl
28	489	87.2	127	15	US-10-462-062-179	Sequence 179, App
29	489	87.2	127	16	US-10-472-905A-119	Sequence 119, App
30	489	86.8	107	16	US-10-462-062-101	Sequence 101, Appl
31	487	86.8	107	15	US-10-472-905A-90	Sequence 90, Appl
32	487	86.8	107	15	US-10-462-062-109	Sequence 109, App
33	487	86.8	107	16	US-10-472-905A-98	Sequence 98, Appl
34	487	86.8	127	15	US-10-462-062-181	Sequence 181, App
35	487	86.8	127	15	US-10-462-062-183	Sequence 183, App
36	487	86.8	127	16	US-10-472-905A-121	Sequence 121, App
37	487	86.8	127	16	US-10-472-905A-123	Sequence 123, App
38	485	86.5	107	15	US-10-412-406-4	Sequence 4, Appli
39	483	86.1	107	16	US-10-412-406-6	Sequence 6, Appli
40	482	85.9	107	14	US-10-340-189-26	Sequence 26, Appl
41	482	85.9	107	15	US-10-325-696-26	Sequence 26, Appl
42	473	84.3	107	9	US-09-797-481-2	Sequence 2, Appli
43	473	84.3	142	9	US-09-844-736-4	Sequence 4, Appli
44	473	84.3	142	14	US-10-162-396-4	Sequence 4, Appli
45	473	84.3	142	17	US-10-819-493-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-774-076-14

; Sequence 14, Application US/10774076
; Publication No. US20040210004A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUSO1
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-774-076-14

Query Match   100.0%; Score 561; DB 17; Length 107;
Best Local Similarity   100.0%;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
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RESULT 2

US-10-774-076-19
; Sequence 19, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 19
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-774-076-19

Query Match   100.0%; Score 561; DB 17; Length 127;
Best Local Similarity   100.0%; Pred. No. 1.9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 80

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||||||||||||||||||||||||||||||||||||||||||
Db   81 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 127

RESULT 3
US-09-158-120A-20
; Sequence 20, Application US/09158120A
; Patent No. US20020102257A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; TITLE OF INVENTION: Respiratory Syncytical Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: P160
; OPERATING SYSTEM: Windows95
; SOFTWARE: MS Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,120A
; FILING DATE: September 21, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,592
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 469201-367
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 AMINO ACID
; TYPE: AMINO ACIDS
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-158-120A-20

Query Match   90.9%; Score 510; DB 9; Length 107;
Best Local Similarity   88.8%; Pred. No. 3.7e-36;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       ||||||||||||||||||||||||||||:|:||||||||:|||||||||||||||||||
Db   1 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||||||||||||:|||||||||||||||||||||||||:|||
Db   61 RFSGSGSGTFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 107

RESULT 4
US-10-774-076-3
; Sequence 3, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-3

Query Match   89.7%; Score 503; DB 17; Length 107;
Best Local Similarity   87.9%; Pred. No. 1.4e-35;
Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       ||||||||||||||||||||||||||||:|:||||||||:||||||:|||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||||||:|||||||||||||||||||||||||||||||:|||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107

RESULT 5
US-10-774-076-11
; Sequence 11, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-11

US-10-340-189-27

Query Match   89.7%; Score 503; DB 17; Length 127;
Best Local Similarity   87.9%; Pred. No. 1.7e-35;
Matches 94; Conservative   8; Mismatches   5; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       ||:||||||:.|||:|:||||||||||||||||||||||||:||||||||||||||||
Db 21 DIKMTQSPSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 80

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||||::.|||||:.||:|:|||||||||||||||||||:|||
Db 81 RFSGSGSGQDVSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 127

RESULT 6
US-10-340-189-27
Sequence 27, Application US/10340189
Publication No. US20030229207A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-340-189-27

Query Match   89.5%; Score 502; DB 14; Length 107;
Best Local Similarity   88.8%; Pred. No. 1.8e-35;
Matches 95; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       |||||||||:.|||:||||||||:||||||||||||||||:||||||||||||||||||
Db 1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||||.:||||||||.:||:|.|||||.||..|||||||:|||
Db 61 RFSGSGSGGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

Db 61 RFSGSGSGGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 7
US-10-325-696-27
Sequence 27, Application US/10325696
Publication No. US20040005630A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-325-696-27

Query Match   89.5%; Score 502; DB 15; Length 107;
Best Local Similarity   88.8%; Pred. No. 1.8e-35;
Matches 95; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       |||||||||:.|||:||||||||:||||||||||||||||:||||||||||||||||||
Db 1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
       |||||||||.:||||||||.:||:|.|||||.||..|||||||:|||
Db 61 RFSGSGSGGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 8
US-10-462-062-107
Sequence 107, Application US/10462062
Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

```
;  TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;  FILE REFERENCE: 053466-0360
;  CURRENT APPLICATION NUMBER: US/10/462,062
;  CURRENT FILING DATE: 2003-06-16
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 107
;  LENGTH: 107
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
;  OTHER INFORMATION: for version "b1" of humanized L chain V region
US-10-462-062-107

  Query Match             88.9%;  Score 499;  DB 15;  Length 107;
  Best Local Similarity   89.7%;  Pred. No. 3.2e-35;
  Matches   96;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||:|| |||||||:|| |||:|||||::||||
Db          1 DIQMTQSPSSLSASVGDRVTITCKASQDIKSFLSWFQQKPGKSPKTLIYYATSLADGVPS 60

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
              ||||||||:||||||||||||||||||||:|| ||||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 107


RESULT 9
US-10-472-905A-96
;  Sequence 96, Application US/10472905A
;  Publication No. US2004018051A1
;  GENERAL INFORMATION:
;  APPLICANT: SUZUKI, KOJI
;  TITLE OF INVENTION: BLOOD RHEOLOGY-IMPROVING AGENT
;  FILE REFERENCE: 053466-0368
;  CURRENT APPLICATION NUMBER: US/10/472,905A
;  CURRENT FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: PCT/JP02/02933
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: JP 2001-088387
;  PRIOR FILING DATE: 2001-03-26
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: Patentin Ver. 3.2
;  SEQ ID NO 96
;  LENGTH: 107
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;  OTHER INFORMATION: amino acid sequence of version "b1" of humanized L
US-10-472-905A-96

  Query Match             88.9%;  Score 499;  DB 16;  Length 107;
  Best Local Similarity   89.7%;  Pred. No. 3.2e-35;
  Matches   96;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||:|| |||||||:|| |||:|||||::||||
Db          1 DIQMTQSPSSLSASVGDRVTITCKASQDIKSFLSWFQQKPGKSPKTLIYYATSLADGVPS 60

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
              ||||||||:||||||||||||||||||||:|| ||||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 107


RESULT 10
US-10-462-062-182
;  Sequence 182, Application US/10462062
;  Publication No. US20040044187A1
;  GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: ADACHI, HIDEKI
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;  TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;  FILE REFERENCE: 053466-0360
;  CURRENT APPLICATION NUMBER: US/10/462,062
;  CURRENT FILING DATE: 2003-06-16
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 182
;  LENGTH: 127
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
;  OTHER INFORMATION: sequence of version "b1" of humanized L chain V region
US-10-462-062-182

  Query Match             88.9%;  Score 499;  DB 15;  Length 127;
  Best Local Similarity   89.7%;  Pred. No. 3.8e-35;
  Matches   96;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||:|| |||||||:|| |||:|||||::||||
Db         21 DIQMTQSPSSLSASVGDRVTITCKASQDIKSFLSWFQQKPGKSPKTLIYYATSLADGVPS 80

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
              ||||||||:||||||||||||||||||||:|| ||||||||||||||
Db         81 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 127


RESULT 11
US-10-472-905A-122
;  Sequence 122, Application US/10472905A
;  Publication No. US2004018051A1
;  GENERAL INFORMATION:
;  APPLICANT: SUZUKI, KOJI
;  TITLE OF INVENTION: BLOOD RHEOLOGY-IMPROVING AGENT
;  FILE REFERENCE: 053466-0368
;  CURRENT APPLICATION NUMBER: US/10/472,905A
;  CURRENT FILING DATE: 2003-09-25
;  PRIOR APPLICATION NUMBER: PCT/JP02/02933
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: JP 2001-088387
;  PRIOR FILING DATE: 2001-03-26
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: Patentin Ver. 3.2
;  SEQ ID NO 122
;  LENGTH: 127
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;  OTHER INFORMATION: humanized L chain V region
US-10-472-905A-122

  Query Match             88.9%;  Score 499;  DB 15;  Length 127;
  Best Local Similarity   89.7%;  Pred. No. 3.8e-35;
  Matches   96;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||:|| |||||||:|| |||:|||||::||||
Db         21 DIQMTQSPSSLSASVGDRVTITCKASQDIKSFLSWFQQKPGKSPKTLIYYATSLADGVPS 80

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
              ||||||||:||||||||||||||||||||:|| ||||||||||||||
Db         81 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 127
```

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Db    81 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 127
         ||||:|||| |||||| |||||||| ||||| :| ||||||||||||
Qy       RFSGSGSGTDYTLTISSLQPEDFGIYYCQQYDESPWTFGGGTKLEIK 127
```

RESULT 12
US-10-127-890-125
; Sequence 125, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
;   APPLICANT: Better, Marc D.
;   Carroll, Stephen F.
;   Studnika, Gary M.
;   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;   Proteins
;   NUMBER OF SEQUENCES: 173
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;   STREET: 500 West Madison Street, 34th Floor
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60661
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/127,890
;   FILING DATE: 23-Apr-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/646,360
;   FILING DATE: 13-MAY-1996
;   APPLICATION NUMBER: PCT/US94/05348
;   FILING DATE: 12-MAY-1994
;   APPLICATION NUMBER: US 08/064,691
;   FILING DATE: 12-MAY-1993
;   APPLICATION NUMBER: US 07/988,430
;   FILING DATE: 09-DEC-1992
;   APPLICATION NUMBER: US 07/901,707
;   FILING DATE: 19-JUN-1992
;   APPLICATION NUMBER: US 07/787,567
;   FILING DATE: 04-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McNicholas, Janet M.
;   REGISTRATION NUMBER: 32,918
;   REFERENCE/DOCKET NUMBER: 200-70.P4
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312/707-8889
;   TELEFAX: 312/707-9155
;   TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 125:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-10-127-890-125

Query Match   88.8%; Score 498; DB 14; Length 107;
Best Local Similarity   89.7%; Pred. No. 3.9e-35;
Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
          ||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||:||
Db   1 DIQMTQSPSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
          ||||||||| ||||||||||||||| ||||:|:||:|||||||||||
Db   61 RFSGSGSGTDYTLTISSLQPEDFGIYYCQQYDESPWTFGGGTKLEIK 107
```

RESULT 13
US-10-340-189-87
; Sequence 87, Application US/10340189
; Publication No. US20030229207A1
; GENERAL INFORMATION:
;   APPLICANT: Studnicka, Gary M.
;   TITLE OF INVENTION: Modified Antibody Variable Domains
;   NUMBER OF SEQUENCES: 89
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;     STREET: 500 W. Madison Street, 34th Floor
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60661
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/245,202A
;     FILING DATE: <Unknown>
;     APPLICATION NUMBER: 08/082,842
;     FILING DATE: 23-JUN-1993
;     APPLICATION NUMBER: US 07/808,464
;     FILING DATE: 13-DEC-1991
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/340,189
;     FILING DATE: 10-Jan-2003
;     CLASSIFICATION: 530
;     APPLICATION NUMBER: PCT/US92/10906
;     FILING DATE: 14-DEC-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McNicholas, Janet M.
;     REGISTRATION NUMBER: 32,918
;     REFERENCE/DOCKET NUMBER: 110235U507 / 200-71.P2.C2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/707-8889
;     TELEFAX: 312/707-9155
;     TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 87:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 107 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-10-340-189-87

Query Match             88.8%;  Score 498;  DB 14;  Length 107;
Best Local Similarity   89.7%;  Pred. No. 3.9e-35;
Matches   96;  Conservative   3;  Mismatches   8;  Indels   0;  Gaps   0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60
          ||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||:||
Db      1 DIQMTQSPSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPS  60

Qy     61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
          ||||||||| ||||||||||||||| ||||:|:||:|||||||||||
Db     61 RFSGSGSGTDYTLTISSLQPEDFGIYYCQQYDESPWTFGGGTKLEIK 107
```

RESULT 14
US-10-325-696-65
; Sequence 65, Application US/10325696
; Publication No. US20040005630A1
; GENERAL INFORMATION:
;   APPLICANT: Studnicka, Gary M.
;   TITLE OF INVENTION: Modified Antibody Variable Domains
;   NUMBER OF SEQUENCES: 67
```

; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-436-782-33

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Query Match      88.4%;    Score 496;   DB 15;   Length 107;
Best Local Similarity  86.0%;  Pred. No. 5.7e-35;
Matches  92;  Conservative  10;  Mismatches  5;  Indels  0;  Gaps  0;

Qy    1  DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60
         |||:||||||:.||:.|.:|||||||||||||||||||||||:|||||||||||||||||
Db    1  DIKMTQSPSSMYASLGERVTITCRASQDINNYLSWFQQKPGKSPKTLIYRANRLESGVPS  60

Qy   61  RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK  107
         |||||||||:|::||||||:.|| .|:||||||||||||||||.|:||
Db   61  RFSGSGSGDYSLTISSLEYEDMGIYYCLKYDEFPYTFGGGTKLEIK  107
```

Search completed: December 29, 2004, 18:42:01
Job time : 62.8643 secs

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-325-696-65

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Query Match      88.8%;    Score 498;   DB 15;   Length 107;
Best Local Similarity  89.7%;  Pred. No. 3.9e-35;
Matches  96;  Conservative  3;  Mismatches  8;  Indels  0;  Gaps  0;

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Qy   61  RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK  107
         |||||||||:|:.||||||:.|||| .|:| ||||||||||||.|:||
Db   61  RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK  107
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RESULT 15
US-10-436-782-33
Sequence 33, Application US/10436782
Publication No. US20040028685A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kiener, Peter
APPLICANT: Langermann, Solomon
TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-097
CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,322
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2003-04-03

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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:         December 29, 2004, 17:37:57 ; Search time 73.5428 Seconds
                                             (without alignments)
                                             521.928 Million cell updates/sec

Title:          US-10-774-076-14
Perfect score:  561
Sequence:       1 DIQMTQSPSSLSASVGDRVT...........CLQYDEFPYTFGGGTKVEIK 107

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched:       2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters:      2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :
         1: A_Geneseq_23Sep04:*
         2: geneseqp1980s:*
         3: geneseqp1990s:*
         4: geneseqp2000s:*
         5: geneseqp2001s:*
         6: geneseqp2002s:*
         7: geneseqp2003as:*
         8: geneseqp2003bs:*
            geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	%Query Match	Length	DB	ID	Description
1	520	92.7	107	2	Aaw23953	Chimeric
2	520	92.7	240	2	Aaw23954	Chimeric
3	514	91.6	107	6	Abg74710	Murine hu
4	514	91.6	107	7	Abr83157	Hu007 ant
5	514	91.6	214	7	Abg74711	Murine hu
6	514	91.6	214	7	Abr83150	Hu007 ant
7	510	90.9	107	2	Aar92082	Murine 13
8	510	90.9	107	2	Abg31429	Humanised
9	510	90.9	129	2	Aar57482	Humanised
10	510	90.9	129	2	Aar92085	Humanised
11	510	90.9	129	2	Abg31444	Amino aci
12	502	89.5	107	2	Aaw58478	Humanised
13	502	89.5	107	8	Adi01168	Murine mo
14	499	88.9	107	4	Aay52724	Humanised
15	499	88.9	107	6	Aab74985	Humanised
16	499	88.9	127	6	Aao16815	Blood flo
17	498	88.8	107	2	Aar41283	Moderate-
18	498	88.8	107	2	Aaw58515	Protein S
19	498	88.8	107	8	Adi01228	Murine mo
20	496	88.4	107	8	Ade85729	Human Eph
21	496	88.4	107	8	Adl23067	Human Eph
22	494	88.1	237	7	Ade57549	Human Pro
23	494	88.1	237	7	Add47098	Human Pro
24	494	88.1	237	7	Add48668	Human Pro
25	494	88.1	246	4	Aab86037	Murine an
26	493	87.9	107	2	Aay52722	Humanised
27	493	87.9	107	2	Aab74983	Humanised
28	493	87.9	127	6	Aao16813	Blood flo
29	491	87.5	107	5	Aao18394	Humanised
30	491	87.5	214	5	Aaw27089	Mouse mon
31	491	87.5	214	5	Aao18399	Mature hu
32	491	87.5	355	2	Aaw35125	R. pipien
33	491	87.5	355	2	Aaw35129	R. pipien
34	491	87.5	358	2	Aaw35127	R. pipien
35	491	87.5	358	2	Aaw35130	R. pipien
36	491	87.5	360	2	Aaw35128	R. pipien
37	491	87.5	379	2	Aaw35126	R. pipien
38	489	87.2	107	2	Aay52721	Humanised
39	489	87.2	107	2	Aab74982	Humanised
40	489	87.2	107	6	Aao16821	Blood flo
41	489	87.2	127	6	Aao16812	Blood flo
42	487	86.8	107	2	Aay52723	Humanised
43	487	86.8	107	2	Aay52725	Humanised
44	487	86.8	107	4	Aab74984	Humanised
45	487	86.8	107	4	Aab74986	Humanised

ALIGNMENTS

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RESULT 1
AAW23953
ID   AAW23953 standard; protein; 107 AA.
XX
AC   AAW23953;
XX
DT   17-OCT-2003  (revised)
DT   17-JUN-1998  (first entry)
XX
DE   Chimeric humanised Mus musculus A717 antibody heavy chain.
XX
KW   Chimeric; humanised; human; murine; A717; antibody; heavy chain;
KW   variable region; diabetes; prophylactic treatment.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO9749429-A1.
XX
PD   31-DEC-1997.
XX
PF   26-JUN-1996;  97WO-US011605.
XX
PR   27-JUN-1996;  96US-00672176.
XX
PA   (EXOC-) EXOCELL INC.
XX
PI   Cohen MP,  Shearman CW;
XX
DR   WPI; 1998-076916/07.
DR   N-PSDB; AAV04637.
XX
PT   New humanised antibodies specific for glycated albumin - prepared by
PT   recombinant expression of humanised mouse antibodies, useful for, e.g.
PT   treating diabetic vasculopathy.
XX
PS   Example 2; Page 15; 27pp; English.
XX
CC   The sequence is that of a humanised variable region of the A717 antibody
CC   light chain VL-1. The antibody has specificity for glycated albumin (GA)
CC   and is capable of neutralising the effects of GA in vivo. It can be used
CC   in the manufacture of therapeutics useful for the prophylactic treatment
CC   of complications of diabetes (especially diabetic vasculopathy and
CC   retinopathy) and atherosclerotic cardiovascular disease. The genetically
CC   engineered antibodies are specific as they only interact with GA but not
CC   other proteins and may be easily prepared in pure form. (Updated on 17-
CC   OCT-2003 to standardise OS field)
```

```
XX
SQ   Sequence 107 AA;

Qy   Query Match    92.7%;  Score 520;  DB 2;  Length 107;
     Best Local Similarity    92.5%;  Pred. No. 8.5e-33;
     Matches  99;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKSLIYHTNRLLDGVPS  60
          ||||||||||||||||||||||||||||||||||||||||||||||||| :||||
Db      1 DIQMTQSPSSLSASVGDRVTITCKASQDIDSYLSWFQQKPGKAPKSLIYHTNRLLDGVPS  60

Qy     61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
          |||||||||||||||||||||||||||||||||||| |||||||||
Db     61 RFSGSGSGTDFTLTISSLQPEDFATYYCLQYDEFPITFGGGTIKVEIK 107

Qy
Db

RESULT 2
ID   AAW23954 standard; protein; 240 AA.
XX
DE   Chimeric humanised Mus musculus A717 antibody ScFv.
XX
KW   Chimeric; humanised; human; murine; A717; antibody; ScFv;
KW   variable region; diabetes; prophylactic treatment.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO9749429-A1.
XX
PD   31-DEC-1997.
XX
DT   17-JUN-1998 (first entry)
DT   17-OCT-2003 (revised)
XX
AC   AAW23954;
XX
ID   AAW23954;
XX
PF   26-JUN-1997; 97WO-US011605.
XX
PR   27-JUN-1996; 96US-0672176.
XX
PA   (EXOC-) EXOCELL INC.
XX
PI   Cohen MP, Shearman CW;
XX
DR   N-PSDB; AAV04638.
DR   WPI; 1998-076916/07.
XX
PT   New humanised antibodies specific for glycated albumin - prepared by
PT   recombinant expression of humanised mouse antibodies, useful for,
PT   treating diabetic vasculopathy.
XX
PS   Example 3; Page 15-16; 27pp; English.
XX
CC   The sequence is that of a humanised variable region of the A717 antibody
CC   ScFv, huA717-ScFv. The antibody has specificity for glycated albumin (GA)
CC   and is capable of neutralising the effects of GA in vivo. It can be used
CC   in the manufacture of therapeutics useful for the prophylactic treatment
CC   of complications of diabetes (especially diabetic vasculopathy and
CC   retinopathy) and atherosclerotic cardiovascular disease. The genetically
CC   engineered antibodies are specific as they only interact with GA but not
CC   other proteins and may be easily prepared in pure form. (Updated on 17-
CC   OCT-2003 to standardise OS field)
XX
SQ   Sequence 240 AA;

Qy   Query Match    92.5%;  Score 520;  DB 2;  Length 240;
     Best Local Similarity    92.5%;  Pred. No. 1.8e-32;
     Matches  99;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKSLIYHTNRLLDGVPS  60
          ||||||||||||||||||||||||||||||||||||||||||||||||| :||||
Db    134 DIQMTQSPSSLSASVGDRVTITCKASQDIDSYLSWFQQKPGKAPKSLIYHTNRLLDGVPS 193

Qy     61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
          |||||||||||||||||||||||||||||||||||| |||||||||
Db    194 RFSGSGSGTDFTLTISSLQPEDFATYYCLQYDEFPITFGGGTIKVEIK 240

Qy
Db
```

```
RESULT 3
ID   ABG74710 standard; protein; 107 AA.
XX
AC   ABG74710;
XX
DT   10-MAY-2003 (first entry)
XX
DE   Murine.humanised Mu007 light chain variable region.
XX
KW   Murine; light chain; variable region; antibody; Crohn's disease;
KW   human interleukin (IL)-1beta; antibody; anti-rheumatic; humanised;
KW   antiinflammatory; osteopathic; antiallergic; antiarthritic; humanised;
KW   antiasthmatic; immunosuppressive; antibacterial; vaccine; Mu007;
KW   rheumatoid arthritis; osteoarthritis; cartilage destruction; allergy;
KW   septic shock; endotoxic shock; septicaemia; stroke; asthma;
KW   graft versus host disease; inflammatory bowel disease.
XX
OS   Mus musculus.
OS   Synthetic.
XX
PN   WO2003010282-A2.
XX
PD   06-FEB-2003.
XX
DT   18-JUL-2002; 2002WO-US021281.
XX
PR   26-JUL-2001; 2001US-0307973P.
PR   14-AUG-2001; 2001US-0312278P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bright SW, Jia AY, Kuhstoss SA, Manetta JV, Tsurushita N,
PI   Vasquez MJ;
XX
DR   N-PSDB; ABQ77443.
DR   WPI; 2003-240068/24.
XX
PT   New IL-1beta antibodies, useful for treating allergy, septic or endotoxic
PT   shock, septicemia, stroke, asthma, graft versus host disease, Crohn's
PT   disease, or inflammatory bowel disease.
XX
PS   Disclosure; Page 70-71; 98pp; English.
XX
CC   This invention describes a novel antibody that specifically binds mature
CC   human interleukin (IL)-1beta, and binds the same epitope on mature human
CC   IL-1beta as mouse monoclonal antibody Mu007 or humanised antibody Hu007.
CC   The antibody of the invention have antirheumatic,
CC   antiinflammatory, osteopathic, antiallergic, antiarthritic,
CC   antiasthmatic, immunosuppressive, antiallergic, cereoprotective,
CC   used in a vaccine. The antibody is useful for manufacturing a medicament
CC   for treating rheumatoid arthritis or osteoarthritis, or for inhibiting
CC   cartilage destruction in a subject. The antibody is also useful for
CC   treating allergy, septic or endotoxic shock, septicaemia, stroke,
CC   graft versus host disease, Crohn's disease, or inflammatory bowel
CC   disease. This sequence represents the humanised murine Mu007 light chain
CC   variable region described in the disclosure of the invention
XX
SQ   Sequence 107 AA;

Qy   Query Match    91.6%;  Score 514;  DB 6;  Length 107;
     Best Local Similarity    91.6%;  Pred. No. 2.5e-32;
     Matches  98;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60
          |||||||||||||||||||||||||||||||||||||||||||||| :||| ||||||
```

Db 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKSLIYRVKRLVDGVPS 60
Qy 1 |||||||||||||||||||||||||||| ||||||||||| ||:|||
Db 61 RFSGSGSGGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGGTKVEIK 107

Qy 61 RFSGSGSGGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGGTKVEIK 107
       ||||| || ||||||||||||| ||||||||||||||||| ||:|||
Db 61 RFSGSASGTDYTLTISSLQPEDFPATYYCLQYDEFPYTFGQGTKLEIK 107

RESULT 4
ABR83157
ID   ABR83157 standard; protein; 107 AA.
XX
AC   ABR83157;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Hu007 antibody light chain variable region sequence.
XX
KW   Hu007; analogue; humanized antibody; IL-1beta; interleukin-1 beta;
KW   complementarity determining region; osteopathic; antiarthritic;
KW   gene therapy; CDR; human.
XX
OS   Homo sapiens.
XX
XX
XX
PN   WO2003073982-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US003117.
XX
PR   28-FEB-2002; 2002US-0361423P.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Beals JM, Huang L, Lu J, Rogers DP, Witcher DR;
XX
DR   WPI; 2003-731644/69.
XX
PT   New analog of humanized antibody Hu007 that specifically binds mature IL-
PT   1 beta, useful for the manufacture of a medicament for treating
PT   rheumatoid arthritis or osteoarthritis.
XX
PS   Disclosure; Fig 1; 120pp; English.
XX
CC   The invention relates to an analogue of humanized antibody Hu007 that
CC   specifically binds mature IL-1beta and comprises at least one amino acid
CC   substitution at positions 54, 55 or 56 of the heavy chain complementarity
CC   determining region 2 (CDR2). The analogue is useful for the manufacture
CC   of a medicament for treating rheumatoid arthritis or osteoarthritis or
CC   for inhibiting cartilage destruction. The present sequence represents an
CC   antibody Hu007 light chain variable region
XX
SQ   Sequence 107 AA;

Query Match   91.6%; Score 514; DB 7; Length 107;
Best Local Similarity   91.6%; Pred. No. 2.5e-32;
Matches   98; Conservative   3; Mismatches   6; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       |||||||||||||||||||||||||||| ||||||||||| ||:|||
Db 1 DIQMTQSPSSLSASVGDRVTITCKASQDIDRYLSWFQQKPGKAPKSLIYRVKRLVDGVPS 60

Qy 61 RFSGSGSGGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGGTKVEIK 107
       ||||| || ||||||||||||| ||||||||||||||||| ||:|||
Db 61 RFSGSASGTDYTLTISSLQPEDFPATYYCLQYDEFPYTFGQGTKLEIK 107

RESULT 5
ABG74711
ID   ABG74711 standard; protein; 214 AA.
XX
AC   ABG74711;
XX
DT   10-MAY-2003 (first entry)
XX
DE   Murine humanised Mu007 light chain variable region #2.
XX
KW   Murine; light chain; variable region; antibody; Crohn's disease;
KW   human interleukin (IL)-1beta; antirheumatic; antiarthritic; humanised;
KW   antiinflammatory; osteopathic; antiallergic; cerebroprotective;
KW   antiasthmatic; immunosuppressive; antibacterial; vaccine; Mu007;
KW   rheumatoid arthritis; osteoarthritis; cartilage destruction; allergy;
KW   septic shock; endotoxic shock; septicaemia; stroke; asthma;
KW   graft versus host disease; inflammatory bowel disease.
XX
OS   Mus musculus.
OS   Synthetic.
XX
PN   WO2003010282-A2.
XX
PD   06-FEB-2003.
XX
PF   18-JUL-2002; 2002WO-US021281.
XX
PR   26-JUL-2001; 2001US-0307973P.
PR   14-AUG-2001; 2001US-0312278P.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Bright SW, Jia AY, Kuhstoss SA, Manetta JV, Tsurushita N;
PI   Vasquez MJ;
XX
DR   WPI; 2003-248068/24.
DR   N-PSDB; ABQ77444.
XX
PT   New IL-1beta antibodies, useful for treating allergy, septic or endotoxic
PT   shock, septicaemia, stroke, asthma, graft versus host disease, Crohn's
PT   disease, or inflammatory bowel disease.
XX
PS   Disclosure; Page 75-76; 98pp; English.
XX
CC   This invention describes a novel antibody that specifically binds mature
CC   human interleukin (IL)-1beta, and binds the same epitope on mature human
CC   IL-1beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.
CC   The antibody of the invention have antirheumatic, antiarthritic,
CC   antiinflammatory, osteopathic, antiallergic, cerebroprotective,
CC   antiasthmatic, immunosuppressive and antibacterial activity and can be
CC   used in a vaccine. The antibody is useful for manufacturing a medicament
CC   for treating rheumatoid arthritis or osteoarthritis, or for inhibiting
CC   cartilage destruction in a subject. The antibody is also useful for
CC   treating allergy, septic or endotoxic shock, septicaemia, stroke, asthma,
CC   graft versus host disease, Crohn's disease, or inflammatory bowel
CC   disease. This sequence represents the humanised murine Mu007 light chain
CC   variable region described in the disclosure of the invention
XX
SQ   Sequence 214 AA;

Query Match   91.6%; Score 514; DB 6; Length 214;
Best Local Similarity   91.6%; Pred. No. 4.8e-32;
Matches   98; Conservative   3; Mismatches   6; Indels   0; Gaps   0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
       |||||||||||||||||||||||||||| ||||||||||| ||:|||
Db 1 DIQMTQSPSSLSASVGDRVTITCKASQDIDRYLSWFQQKPGKAPKSLIYRVKRLVDGVPS 60

Qy 61 RFSGSGSGGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGGTKVEIK 107
       ||||| || ||||||||||||| ||||||||||||||||| ||:|||
Db 61 RFSGSASGTDYTLTISSLQPEDFPATYYCLQYDEFPYTFGQGTKLEIK 107

RESULT 6
ABR83150
ID   ABR83150 standard; protein; 214 AA.
XX
AC   ABR83150;
XX
DT   15-JAN-2004 (first entry)

XX
DE   Hu007 antibody analogue light chain sequence.
XX
KW   gene therapy; CDR.
KW   complementarity determining region; osteopathic; antiarthritic;
KW   Hu007; analogue; humanized antibody; IL-1beta; interleukin-1 beta;
XX
OS   Synthetic.
XX
XX
PN   WO200307982-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US003117.
XX
PR   28-FEB-2002; 2002US-0361423P.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Beals JM, Huang L, Lu J, Rogers DP, Witcher DR;
XX
DR   WPI; 2003-731644/69.
DR   N-PSDB; ACF57836.
XX
PT   New analog of humanized antibody Hu007 that specifically binds mature IL-
PT   1 beta, useful for the manufacture of a medicament for treating
PT   rheumatoid arthritis or osteoarthritis.
XX
PS   Claim 17; Page 13-14; 120pp; English.
XX
CC   The invention relates to an analogue of humanized antibody Hu007 that
CC   specifically binds mature IL-1beta and comprises at least one amino acid
CC   substitution at positions 54, 55 or 56 of the heavy chain complementarity
CC   determining region 2 (CDR2). The analogue is useful for the manufacture
CC   of a medicament for treating rheumatoid arthritis or osteoarthritis or
CC   for inhibiting cartilage destruction. The present sequence represents an
CC   antibody Hu007 analogue light chain sequence
XX
SQ   Sequence 214 AA;

Query Match   91.6%; Score 514; DB 7; Length 214;
Best Local Similarity   91.6%; Pred. No. 4.8e-32;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
           ||||||||||||||||||||||||||||||||||||||||||:||| ||:||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKASQDIDRYLSWFQQKPGKAPKSLIYRVKRLVDGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
           |||||||||||||||||||||||||||||||:|||||||||| |||
Db   61 RFSGSASGTDYTLTISSLQPEDFATYYCLQYDEPPYTFGQGTKLEIK 107

RESULT 7
AAR92082
ID   AAR92082 standard; protein; 107 AA.
AC   AAR92082;
XX
DT   16-OCT-2003 (revised)
DT   15-MAY-1996 (first entry)
XX
DE   Murine 1308F VL CDR-grafted K102 VL.
XX
KW   Humanised antibody; chimeric antibody; antibody engineering;
KW   monoclonal antibody; MAb 1308F; respiratory syncytial virus; RSV;
KW   light chain; complementarity determining region; CDR.
XX
OS   Homo; sapiens.
OS   Mus musculus.
OS   Chimeric.
XX
FH   Key   Location/Qualifiers

FT   Region   24...34
FT   /label= CDR1
FT   Region   50...56
FT   /label= CDR2
FT   Region   89...97
FT   /label= CDR3
XX
PN   WO9605229-A1.
XX
PD   22-FEB-1996.
XX
PF   09-AUG-1995; 95WO-US010053.
XX
PR   15-AUG-1994; 94US-00290592.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Johnson LS;
XX
DR   WPI; 1996-139646/14.
XX
PT   New chimeric antibodies against respiratory syncytial virus - comprise
PT   human antibodies with CDR's from the variable heavy and light chains of a
PT   murine antibody.
XX
PS   Example 2; Fig 2A-2B; 55pp; English.
XX
CC   A human-mouse chimeric antibody light chain has a human K102 framework
CC   contg. complementarity determining regions (CDRs) from the variable light
CC   (VL) chain of a murine monoclonal antibody (MAb 1308F) against
CC   respiratory syncytial virus (RSV) glycoprotein F antigenic site C. CDRs
CC   from MAb 1308 VL (AAR92083) were grafted into the human HV3 VL region
CC   (AAR92081) to produce CDR-grafted VL (AAR92082). A similar procedure was
CC   used to obtain CDR-grafted VH (AAR92079). The humanised antibody is used
CC   to treat RSV infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 107 AA;

Query Match   90.9%; Score 510; DB 2; Length 107;
Best Local Similarity   88.8%; Pred. No. 5e-32;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
           ||||||||||||||||||||||||||||||:|||||:|||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
           |||||||:|||:|||||||||:|||||||| :|||||||||||:|||
Db   61 RFSGSGSGTEFTLTISSLQPDDFATYYCLQFHFPYTFGGGTKLEIK 107

RESULT 8
ABG31429
ID   ABG31429 standard; protein; 107 AA.
AC   ABG31429;
XX
DT   29-NOV-2002 (first entry)
XX
DE   Humanised CDR-grafted anti-RSV F glycoprotein VL #1.
XX
KW   Human-murine chimeric antibody; humanised antibody; CDR;
KW   complementarity determining region; variable heavy chain; VH;
KW   variable light chain; VL; monoclonal antibody; MAb; RSV infection;
KW   respiratory syncytial virus infection; virucide; human; CDR-grafted;
KW   K102; anti-RSV F glycoprotein VL; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
PN   US20021022657-A1.

XX
PD   01-AUG-2002.
XX
PF   21-SEP-1998;   98US-00158120.
XX
PR   21-SEP-1998;   98US-00158120.
XX
PA   (JOHN/) JOHNSON L S.
XX
PI   Johnson LS;
XX
DR   WPI; 2002-673988/72.
XX
PS   Example 2; Fig 2; 33pp; English.
XX
PT   New human-murine chimeric antibody useful for preventing or treating
PT   respiratory syncytial viral (RSV) infection, contains at least one
PT   complementarity determining region from a murine antibody.
XX
CC   The present invention relates to a human-murine chimeric antibody
CC   comprising a human antibody containing at least one complementarity
CC   determining region (CDR) from each of the variable heavy (VH) and
CC   variable light (VH) chains of a non-human, preferably murine, monoclonal
CC   antibody (MAb) against respiratory syncytial virus (RSV). The humanised
CC   antibody is useful for preventing or treating a respiratory syncytial
CC   virus infection. The antibody is also useful for diagnosing RSV
CC   infection. The antibody can be injected which is preferable to prior art
CC   treatment methods involving intravenous transfusions. The present
CC   sequence represents a human-murine chimeric antibody
XX
SQ   Sequence 107 AA;

Query Match   90.9%; Score 510; DB 5; Length 107;
Best Local Similarity   88.8%; Pred. No. 5e-32;
Matches   95; Conservative   8; Mismatches   4; Indels   0; Gaps   0;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
        ||||||||| ||||||||||||||||||||:|||: ||:|||:|||||||||||||||||
Db   1 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 60

Qy  61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
        |||||||| :|||||||||| ||||||||||: ||||||||||:||| 
Db  61 RFSGSGSGTEFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 107
```

RESULT 9
AAR57482
ID   AAR57482 standard; protein; 129 AA.
AC   AAR57482;
XX
DT   25-MAR-2003 (revised)
DT   02-OCT-1995 (first entry)
XX
DE   Humanized 1308F VL.
XX
KW   Monoclonal antibody; MAb; respiratory syncytial virus; RSV;
KW   chimeric antibody; humanized antibody; antibody engineering; light chain;
KW   VL; complementarity determining region; CDR.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Region   46..54
FT   /label= CDR1
FT   Region   72..78
FT   /label= CDR2
FT   Region   111..119
FT   /label= CDR3
XX
PN   WO9417105-A1.
XX
PD   04-AUG-1994.
XX

XX
PF   29-JAN-1993;   93WO-US001168.
XX
PR   29-JAN-1993;   93WO-US001168.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Johnson L;
XX
DR   WPI; 1994-264037/32.
DR   N-PSDB; AAQ67194.
XX
PS   Disclosure; Fig 4A-4B; 34pp; English.
XX
PT   Human-murine chimeric antibodies against respiratory syncytial virus -
PT   comprises at least 1 CDR from each variable heavy and light chain of at
PT   least 1 murine monoclonal antibody.
XX
CC   Synthetic overlapping oligonucleotides and the 5' primer given in
CC   (AAQ67197) and 3' primer of (AAQ67198) were used to construct a DNA sequence
CC   (AAQ67194) encoding humanized 1308F VL (AARS7482) in which CDRs of the
CC   anti-RSV F antigen murine Mab 1308F VL region were substituted into the
CC   homologous human K102 gene. Similar procedures were used to obtain
CC   humanized 1308F VH for the construction of anti-RSV F protein humanized
CC   antibody. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 129 AA;

Query Match   90.9%; Score 510; DB 2; Length 129;
Best Local Similarity   88.8%; Pred. No. 6e-32;
Matches   95; Conservative   8; Mismatches   4; Indels   0; Gaps   0;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
        ||||||||| ||||||||||||||||||||:|||: ||:|||:|||||||||||||||||
Db  23 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 82

Qy  61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
        |||||||| :|||||||||| ||||||||||: ||||||||||:||| 
Db  83 RFSGSGSGTEFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 129
```

RESULT 10
AAR92085
ID   AAR92085 standard; protein; 129 AA.
AC   AAR92085;
XX
DT   15-MAY-1996 (first entry)
XX
DE   Humanised antibody 1308 VL.
XX
KW   Humanised antibody; chimeric antibody; antibody engineering;
KW   monoclonal antibody; MAb 1308F; respiratory syncytial virus; RSV;
KW   light chain; complementarity determining region; CDR.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Region   46..55
FT   /label= CDR1
FT   Region   72..78
FT   /label= CDR2
FT   Region   111..119
FT   /label= CDR3
XX
PN   WO9605229-A1.
XX
PD   22-FEB-1996.
XX
PF   09-AUG-1995;   95WO-US010053.
XX
PR   15-AUG-1994;   94US-00290592.
XX

PA (MEDI-) MEDIMMUNE INC.
XX
PI Johnson LS;
XX
DR WPI; 1996-139646/14.
DR N-PSDB; AAT16181.
XX
PT New chimeric antibodies against respiratory syncytial virus - comprise human antibodies with CDR's from the variable heavy and light chains of a murine antibody.
XX
PS Example 2; Fig 4A-4B; 55pp; English.
XX
CC A human-mouse chimeric antibody light chain has a human HV3 framework
CC contg. complementarity determining regions (CDRs) from the variable light
CC (VL) chain of murine monoclonal antibody (MAb) 1308F active against
CC respiratory syncytial virus (RSV) glycoprotein F antigenic site C. DNA
CC (AAT16181) coding for CDR-grafted VL-encoding region, Hu1308 VL
CC (AAR92085), was synthesized using overlapping oligonucleotides. The
CC construct was used with Hu1308 VH (see AAR92084) for prodn. in COS-1
CC transfectants of humanised antibody useful for treatment of RSV infection
XX
SQ Sequence 129 AA;

Query Match   90.9%;   Score 510;   DB 2;   Length 129;
Best Local Similarity   88.8%;   Pred. No. 6e-32;
Matches   95;   Conservative   8;   Mismatches   4;   Indels   0;   Gaps   0;

```
Qy  1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
        |||||||||:|||||||||||||||||||||:||:|||||||||:|:||||||||||||
Db 23 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 82

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDBFPYTFGGGTKVEIK 107
        ||||||||::||||||||||:||||||||||:|:|||||||||:|||
Db 83 RFSGSGSGTBFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 129
```

RESULT 11
ABG31444
ID ABG31444 standard; protein; 129 AA.
XX
AC ABG31444;
XX
DT 29-NOV-2002 (first entry)
XX
DE Amino acid sequence for humanised antibody Hu1308VL.
XX
KW Human-murine chimeric antibody; humanised antibody; CDR;
KW complementarity determining region; variable heavy chain; VH;
KW variable light chain; VL; monoclonal antibody; MAb; RSV infection;
KW respiratory syncytial virus infection; virucide; Hu1308VL;
KW mutein.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
CC Human-murine chimeric antibody useful for preventing or treating
PN US2002102257-A1.
XX
PD 01-AUG-2002.
XX
PF 21-SEP-1998; 98US-00158120.
PR 21-SEP-1998; 98US-00158120.
XX
PA (JOHN/) JOHNSON L S.
XX
PI Johnson LS;
XX
DR WPI; 2002-673988/72.
XX
PT New human-murine chimeric antibody useful for preventing or treating

PT respiratory syncytial viral (RSV) infection, contains at least one
PT complementarity determining region from a murine antibody.
XX
PS Example 2; Fig 4; 33pp; English.
XX
CC The present invention relates to a human-murine chimeric antibody
CC comprising a human antibody containing at least one complementarity
CC determining region (CDR) from each of the variable heavy (VH) and
CC variable light (VH) chains of a non-human, preferably murine, monoclonal
CC antibody (MAb) against respiratory syncytial virus (RSV). The humanised
CC antibody is useful for preventing or treating a respiratory syncytial
CC virus infection. The antibody is also useful for diagnosing RSV
CC infection. The antibody can be injected which is preferable to prior art
CC treatment methods involving intravenous transfusions. The present
CC sequence represents a human-murine chimeric antibody
XX
SQ Sequence 129 AA;

Query Match   90.9%;   Score 510;   DB 5;   Length 129;
Best Local Similarity   88.8%;   Pred. No. 6e-32;
Matches   95;   Conservative   8;   Mismatches   4;   Indels   0;   Gaps   0;

```
Qy  1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
        |||||||||:|||||||||||||||||||||:||:|||||||||:|:||||||||||||
Db 23 DIQMTQSPSTLSASVGDRVTITCKASQDINRYLNWYQQKPGKAPKLLIYRANRLVDGVPS 82

Qy 61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDBFPYTFGGGTKVEIK 107
        ||||||||::||||||||||:||||||||||:|:|||||||||:|||
Db 83 RFSGSGSGTBFTLTISSLQPDDFATYYCLQFHEFPYTFGGGTKLEIK 129
```

RESULT 12
AAW58478
ID AAW58478 standard; protein; 107 AA.
XX
AC AAW58478;
XX
DT 18-AUG-1998 (first entry)
XX
DE Humanised anti-CD5 immunoglobulin H65 light chain variable region #1.
XX
KW Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW autoimmune disease; rheumatoid arthritis; type I diabetes.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN US5770196-A.
XX
PD 23-JUN-1998.
XX
PF 07-JUN-1995; 95US-00472788.
XX
PR 13-DEC-1991; 91US-00808464.
PR 14-DEC-1992; 92WO-US010906.
PR 23-JUN-1993; 93US-00082842.
XX
PA (XOMA) XOMA CORP.
XX
PI Studnicka GM;
XX
DR WPI; 1998-376744/32.
XX
PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with
PT humanised variable regions.
XX
PS Claim 1; Col 63-64; 77pp; English.
XX
CC A method has been developed of depleting CD5+ cells in an animal. The
CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig

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CC   molecule, and where the modified Ig variable domain comprises an anti-CD5
CC   Ig molecule, and where the modified Ig variable domain comprises at least
CC   one of (a) a modified light chain variable region (see AAW58478 or
CC   AAW58480), and (b) a modified heavy chain variable region (see AAW58479
CC   or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65
CC   light and heavy chain variable domains with low risk amino acid
CC   substitutions [i.e. low risk of reducing antigen-binding specificity]
CC   and AAW58480 and AAW58481 are humanised forms of the H65 light and heavy
CC   chain variable domains with moderate risk amino acid substitutions and
CC   are present in humanised H65 antibody he3 (ATCC HB 11206). The method is
CC   useful for treating autoimmune diseases, especially systemic lupus
CC   erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The
CC   present sequence represents a specifically claimed humanised anti-CD5
CC   immunoglobulin H65 light chain variable region
XX
SQ   Sequence 107 AA;

Query Match             89.5%;
Best Local Similarity   88.8%;    Pred. No. 2.1e-31;
Matches  95; Conservative  6; Mismatches  6; Indels  0; Gaps  0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||:||||:||||||||:|||||||||||||||||:||||||||||||||||| 
Db   1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy  61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||| ||||||||| ::|| |||||||| :|||||||||:||| 
Db  61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 13
ID   ADI01168 standard; protein; 107 AA.
XX
AC   ADI01168;
XX
DT   22-APR-2004 (first entry)
XX
DE   Murine monoclonal antibody H65 humanised light chain VL protein 1.
XX
KW   variable domain; immunosuppressive; dermatological; antidiabetic;
KW   antidiabetic; antithyroid; antipsoriatic; antirheumatic; antiarthritic;
KW   neuroprotective; antiulcer; antianaemic; fungicide; virucide; autoimmune;
KW   systemic lupus erythematosus; lupus nephritis; scleroderma; morphea;
KW   lichen planus; rheumatoid arthritis; spondylarthritis; thyroiditis;
KW   pemphigus vulgaris; diabetes mellitus type 1;
KW   progressive systemic sclerosis; aplastic anaemia; myasthenia gravis;
KW   myositis; polymyositis; dermatomyositis; Sjogren's disease;
KW   collagen vascular; polyarteritis; inflammatory bowel; Crohn's;
KW   ulcerative colitis; multiple sclerosis; psoriasis;
KW   primary biliary cirrhosis; T cell; tissue transplant rejection;
KW   graft versus host disease; viral; fungal infection; murine; mouse;
KW   monoclonal antibody; H65; humanised light chain.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   US2003229207-A1.
XX
PD   11-DEC-2003.
XX
PF   10-JAN-2003; 2003US-00340189.
XX
PR   13-DEC-1991; 91US-00808464.
PR   14-DEC-1992; 92WO-US001906.
PR   23-JUN-1993; 93US-00082842.
PR   05-FEB-1999; 99US-0245202.
XX
PA   (XOMA ) XOMA TECHNOLOGY LTD.
XX
PI   Studnicka GM;
XX
DR   WPI; 2004-042226/04.


XX
PT   Novel protein containing modified variable domain comprising amino acid
PT   sequence modified at low risk positions in heavy or light chain amino
PT   acid residue at corresponding position of native antibody sequence.
XX
PS   Example 6; SEQ ID NO 27; 80pp; English.
XX
CC   The invention relates to a novel protein containing a modified variable
CC   domain comprising an amino acid sequence modified at low risk positions
CC   such that each amino acid residue in a low risk position in the light or
CC   heavy chain variable region sequence of the domain is same as the amino
CC   acid residue at the corresponding position of a selected antibody light
CC   or heavy chain variable region sequence or consensus sequence. The
CC   polypeptide of the invention demonstrates immunosuppressive,
CC   dermatological, antiinflammatory, antidiabetic, antithyroid,
CC   antipsoriatic, antirheumatic, antiarthritic, neuroprotective, antiulcer,
CC   antianaemic, fungicide and virucide activities. The polypeptide may be
CC   useful for treating autoimmune diseases including systemic lupus
CC   erythematosus and lupus nephritis, scleroderma including morphea and
CC   lichen planus, rheumatoid arthritis and spondylarthritis, thyroiditis,
CC   pemphigus vulgaris, diabetes mellitus type 1, progressive systemic
CC   sclerosis, aplastic anaemia, myasthenia gravis, myositis including
CC   polymyositis and dermatomyositis, Sjogren's disease, collagen vascular
CC   disease, polyarteritis, inflammatory bowel disease including Crohn's
CC   disease and ulcerative colitis, multiple sclerosis, psoriasis and primary
CC   biliary cirrhosis. Furthermore, the polypeptide may be utilised for
CC   address other diseases mediated by T cells, such as tissue transplant
CC   rejection and graft versus host disease, as well as diseases caused by
CC   viral or fungal infection. The current sequence is that of the murine
CC   antibody variable domain protein of the invention.
XX
SQ   Sequence 107 AA;

Query Match             89.5%;
Best Local Similarity   88.8%;    Pred. No. 2.1e-31;
Matches  95; Conservative  6; Mismatches  6; Indels  0; Gaps  0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||:||||:||||||||:|||||||||||||||||:||||||||||||||||| 
Db   1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy  61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||| ||||||||| ::|| |||||||| :|||||||||:||| 
Db  61 RFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 14
AAY52724
ID   AAY52724 standard; protein; 107 AA.
XX
AC   AAY52724;
XX
DT   26-JAN-2000 (first entry)
XX
DE   Humanised ATR-5 L chain V region version "b1" protein sequence.
XX
KW   Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW   ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW   disseminated intravascular coagulation; immunogenicity; chimeric.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9951743-A1.
XX
PD   14-OCT-1999.
XX
PF   02-APR-1999; 99WO-JP001768.
XX
PR   03-APR-1998; 98JP-00091850.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
```

PI Sato K, Adachi H, Yabuta N;
XX
DR WPI; 1999-620204/53.
DR N-PSDB; AAZ33089.
XX
PT Humanised antibody recognizing human tissue factor, used for treatment of
PT disseminated intravascular coagulation.
XX
PS Claim 18; Page 259; 291pp; Japanese.
XX
CC The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal
CC recognising human tissue factor (hTF) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC and prevention of thrombotic disease, especially of disseminated
CC intravascular coagulation (DIC). The humanised antibody has the high hTF
CC binding activity of the mouse monoclonal antibody but greatly reduced
CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 107 AA;

Query Match   88.9%; Score 499; DB 2; Length 107;
Best Local Similarity   89.7%;
Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||||||||||||||||||||||:|||||||||||||:||||  ||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKASQDIKSFLSWFQQKPGKSPKTLIYYATSLADGVPS 60

Qy  61 RFSGSGSGQDYTLTITSSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||| |||||||||||||||||||| ||||||||||||||||
Db  61 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 107
```

RESULT 15
AAB74985
ID AAB74985 standard; protein; 107 AA.
XX
AC AAB74985;
XX
DT 16-JUL-2001 (first entry)
XX
DE Humanised ATR-5 L chain V region version b1 SEQ ID NO:96.
XX
KW Mouse; human; humanised; monoclonal antibody; tissue factor; TF;
KW prevention; blood coagulation; tumour; ATR-5; anticoagulant;
KW thrombolytic; infection; venous thrombosis; arterial thrombosis;
KW vascular medial thickening; accelerated blood coagulation; thrombosis;
KW blood vessel thickening.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO200124626-A1.
XX
PD 12-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006802.
XX
PR 01-OCT-1999; 99JP-00281843.
PR 01-OCT-1999; 99JP-00282120.
PR 01-OCT-1999; 99JP-00282134.
PR 01-OCT-1999; 99JP-00282167.
PR 01-OCT-1999; 99JP-00282188.
PR 01-OCT-1999; 99JP-00282192.

XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Saito H, Kitazawa T, Yoshihashi K, Hattori K;
XX
DR WPI; 2001-300135/31.
DR N-PSDB; AAF87914.
XX
PT Mouse model for sustained accelerated blood coagulation and treatment for
PT accelerated blood coagulation, thrombosis and blood vessel thickening.
XX
PS Example; Page 186-187; 202pp; Japanese.
XX
CC The present invention describes an experimental animal model transplanted
CC with animal cells expressing human tissue factor or a fragment of it,
CC with accelerated blood coagulation. Also described are: (1) selecting an
CC animal model; (2) screening for anti-thrombotics; (3) treatment and
CC prevention of accelerated blood coagulation; and (4) polyclonal and
CC monoclonal antibodies or their fragments. The animal model is useful in
CC the search and development of remedies for diseases associated with the
CC sustained acceleration of blood coagulation such as that caused by
CC infection, venous thrombosis, arterial thrombosis and disease caused by
CC vascular medial thickening. Antibodies from the present invention against
CC human tissue factor (TF) (e.g. anti mouse monoclonal antibody ATR-5 and
CC humanised ATR-5) can be used in the treatment and prevention of
CC accelerated blood coagulation, thrombosis and blood vessel thickening.
CC AAF87837 to AAF87917 and AAB74968 to AAB74990 represent nucleotide and
CC protein sequences which are used in the exemplification of the present
CC invention
XX
SQ Sequence 107 AA;

Query Match   88.9%; Score 499; DB 4; Length 107;
Best Local Similarity   89.7%;
Matches   96; Conservative   3; Mismatches   8; Indels   0; Gaps   0;

```
Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||||||||||||||||||||||:|||||||||||||:||||  ||||
Db   1 DIQMTQSPSSLSASVGDRVTITCKASQDIKSFLSWFQQKPGKSPKTLIYYATSLADGVPS 60

Qy  61 RFSGSGSGQDYTLTITSSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         |||||||| |||||||||||||||||||||:  ||||||||||||||||
Db  61 RFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPYTFGGGTKVEIK 107
```

Search completed: December 29, 2004, 17:57:35
Job time : 74.5428 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 17:38:43 ; Search time 73.8584 Seconds
(without alignments)
833.556 Million cell updates/sec

Title:
Perfect Score: 561
Sequence: 1 DIQMTQSPSSLSASVGDRVT............CLQYDFPYTFGGGTKVEIK 107

US-10-774-076-14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	494	88.1	214	2	Q9R1A5	Q9r1a5 mus musculu
2	494	88.1	236	2	Q7TS98	Q7ts98 mus musculu
3	474	84.5	128	1	KV5E_MOUSE	P01637 mus musculu
4	449	80.0	108	1	KV1Y_HUMAN	P80362 homo sapien
5	446	79.5	236	2	Q7Z3Y4	Q7z3y4 homo sapien
6	445	79.3	236	2	Q6GMX8	Q6gmx8 homo sapien
7	444	79.1	236	2	KV1B_HUMAN	P01594 homo sapien
8	444	79.1	236	2	Q7TMK3	Q7tmk3 mus musculu
9	443	79.0	108	1	KV1V_HUMAN	P04430 homo sapien
10	442	78.8	108	1	KV1P_HUMAN	P01608 homo sapien
11	442	78.8	115	1	KV5P_MOUSE	P01638 mus musculu
12	441	78.6	108	1	KV1R_HUMAN	P01610 homo sapien
13	439	78.3	108	1	KV1O_HUMAN	P01607 homo sapien
14	437	77.9	236	2	Q6GMX9	Q6gmx9 homo sapien
15	436.5	77.8	107	2	Q96SA9	Q96sa9 homo sapien
16	435	77.5	108	2	Q9UL70	Q9ul70 homo sapien
17	435	77.5	236	2	Q6PIH7	Q6pih7 homo sapien
18	435	77.5	236	2	Q6GMW1	Q6gmw1 homo sapien
19	435	77.5	236	2	AAH34141	Aah34141 homo sapi
20	433	77.2	108	2	Q9UL77	Q9ul77 homo sapien
21	432	77.0	108	1	KV1H_HUMAN	P01600 homo sapien
22	432	77.0	236	2	Q6GMX0	Q6gmx0 homo sapien
23	427.5	76.2	107	1	KV1D_HUMAN	P01596 homo sapien
24	427	76.1	108	1	KV1A_HUMAN	P01593 homo sapien
25	427	76.1	108	1	KV1G_HUMAN	P01599 homo sapien
26	427	76.1	108	1	KV1M_HUMAN	P01605 homo sapien
27	426	75.9	108	1	KV1L_HUMAN	P01604 homo sapien
28	423	75.4	108	1	KV1S_HUMAN	P01611 homo sapien
29	420	74.9	108	1	KV1E_HUMAN	P01597 homo sapien
30	420	74.9	108	1	KV1F_HUMAN	P01598 homo sapien
31	419	74.7	108	1	KV1Q_HUMAN	P01609 homo sapien
32	418	74.5	108	1	KV1C_HUMAN	P01595 homo sapien
33	416	74.2	129	1	KV1X_HUMAN	P04432 homo sapien
34	414	73.8	108	1	KV1K_HUMAN	P01603 homo sapien
35	414	73.8	108	2	Q9UL79	Q9ul79 homo sapien
36	413	73.6	234	2	Q7Z473	Q7z473 homo sapien
37	408	72.7	129	1	KV1W_HUMAN	P04431 homo sapien
38	408	72.7	108	1	KV1N_HUMAN	P01606 homo sapien
39	403	71.8	236	2	Q6PIT5	Q6pit5 homo sapien
40	403	71.8	236	2	Q9UL81	Q9ul81 homo sapien
41	403	71.8	107	2	Q96PF6	Q96pf6 homo sapien
42	402.5	71.7	116	2	Aah29444	Aah29444 homo sapi
43	402	71.7	236	2	Q6PIH4	Q6pih4 homo sapien
44	402	71.7	236	2	AAH34146	Aah34146 homo sapi
45	401	71.5	108	1	KV5T_MOUSE	P01653 mus musculu

ALIGNMENTS

RESULT 1
Q9R1A5
Q9R1A5
ID   Q9R1A5   PRELIMINARY;   PRT;   214 AA.
AC   Q9R1A5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Kappa light chain of Mab7 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152371; AAD40242.1; -.
PIR; PH1065; PH1065.
DR   PDB; 1AHW; X-ray; D=-.
DR   PDB; 1CIC; X-ray; A/C=1-214.
DR   PDB; 1EO8; X-ray; L-1-210.
DR   PDB; 1K6Q; X-ray; L-1-210.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001356; Homeobox.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; Ig; 1.
DR   PRINTS; PR00024; HOMEOBOX.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER   1   1
FT   NON_TER   214   214
SQ   SEQUENCE   214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match   88.1%;   Score 494; DB 2; Length 214;
Best Local Similarity   86.0%;   Pred. No. 3.5e-43;
Matches 92; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||:|||:||::|:||||||||||||||||||||:|||:||.|||||||||||||||||
Db   1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDFPYTFGGGTKVEIK 107
         ||||||||||:||||||||||:||:|| :|||||||||||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDFPPTFGGGTKLEIK 107

RESULT 2

```
ID   Q7TS98        PRELIMINARY;     PRT;   236 AA.
AC   Q7TS98;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-colorectal carcinoma light chain.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93383497; PubMed=8372513;
RA   Tonge D.W., Hannam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT   "Cloning and characterization of 1116NS19.9 heavy and light chain
RT   cDNAs and expression of antibody fragments in Escherichia coli.";
RL   Year Immunol. 7:56-62(1993).
DR   EMBL; S65921; AAB28160.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  26454 MW;  2C586EBF5EA1OF4C CRC64;

Query Match    88.1%;  Score 494;  DB 2;  Length 236;
Best Local Similarity  86.9%;  Pred. No. 3.9e-43;
Matches   93;  Conservative   8;  Mismatches   6;  Indels   0;  Gaps   0;

Qy      1  DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60
           |||:|||||||:|||:::|||||||||||||||||||||||:|:|||||||||||||||
Db     23  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  82

Qy     61  RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK  107
           |||||||||||:||||||:||||||||||||||||| ||||||:|:|
Db     83  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPRTFGGGTKLEIK  129
```

```
RESULT 3
ID   KV5E_MOUSE     STANDARD;      PRT;   128 AA.
AC   P01637;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region T1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81052342; PubMed=6776411;
RA   Altenburger W., Steinmetz M., Zachau H.G.;
RT   "Functional and non-functional joining in immunoglobulin light chain
RT   genes of a mouse myeloma.";
RL   Nature 287:603-607(1980).
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DR   EMBL; V00772; CAA24150.1; -.
     PIR; A01920; KVMST1.
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DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   Immunoglobulin V region; Signal.
FT   SIGNAL      1     20
FT   CHAIN      21    128    Ig kappa chain V-V region T1.
FT   DOMAIN     21    128    Ig-like.
FT   DOMAIN     21     43    Framework-1.
FT   DOMAIN     44     54    Complementarity-determining-1.
FT   DOMAIN     55     69    Framework-2.
FT   DOMAIN     70     76    Complementarity-determining-2.
FT   DOMAIN     77    108    Framework-3.
FT   DOMAIN    109    117    Complementarity-determining-3.
FT   DOMAIN    118    127    Framework-4.
FT   DISULFID   43    108    By similarity.
FT   NON_TER     1
FT   NON_TER   128
SQ   SEQUENCE   128 AA;  14385 MW;  AFA563D31BB7E05 CRC64;

Query Match    84.5%;  Score 474;  DB 1;  Length 128;
Best Local Similarity  81.3%;  Pred. No. 2.3e-41;
Matches   87;  Conservative  13;  Mismatches   7;  Indels   0;  Gaps   0;

Qy      1  DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60
           |||:||||||:|||:|:||||||||||||||||||||||||:|:|||||||||||||||
Db     21  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  80

Qy     61  RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK  107
           |||||||||||:||||||:|:||  |  ||||||| |||||:|:|:|
Db     81  RFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGGAGTKLELK  127
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RESULT 4
ID   KVIY_HUMAN     STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
RN   [2]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PDB; 1WTL; X-ray; A/B=1-108.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
```

KW   Immunoglobulin V region.
FT   DOMAIN   1   23   Framework-1.
FT   DOMAIN   24   34   Complementarity-determining-1.
FT   DOMAIN   35   49   Framework-2.
FT   DOMAIN   50   56   Complementarity-determining-2.
FT   DOMAIN   57   88   Framework-3.
FT   DOMAIN   89   97   Complementarity-determining-3.
FT   DOMAIN   98   107   Framework-4.
FT   DISULFID   23   88   By similarity.
FT   CONFLICT   30   31   TN -> SD (in Ref. 2).
FT   STRAND   4   7
FT   STRAND   10   13
FT   TURN   15   16
FT   STRAND   19   25
FT   STRAND   30   31
FT   TURN   33   38
FT   STRAND   40   41
FT   TURN   45   49
FT   STRAND   50   52
FT   STRAND   53   54
FT   TURN   56   57
FT   TURN   60   61
FT   STRAND   62   67
FT   TURN   68   69
FT   HELIX   70   75
FT   HELIX   80   82
FT   STRAND   84   90
FT   STRAND   98   98
FT   STRAND   102   106
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match   80.0%; Score 449; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 7.7e-39;
Matches   85; Conservative   9; Mismatches   13; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGGAPKVLIYGASILETGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
           ||||||| |:|:||||||| |||||||||||| | :|:| |||||||||
Db   61 RFSGSGSGTDFTLTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107

RESULT 5
Q72374
ID   Q72Y4;   PRELIMINARY;   PRT;   236 AA.
AC   Q72Y4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Prange C., Carninci P.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS50290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match   79.5%; Score 446; DB 2; Length 236;
Best Local Similarity 79.4%; Pred. No. 3.9e-38;
Matches   85; Conservative   10; Mismatches   12; Indels   0; Gaps   0;

Qy   1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 DIQMTQSPSSLSASVGDVTVTITCRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
           ||||||| |:|:||||||| |||||||||||| | :|:| |||||||||
Db   83 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIK 129

RESULT 6
Q6GMX8
ID   Q6GMX8;   PRELIMINARY;   PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Prange C., Carninci P.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human

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RT   and mouse cDNA sequences.";
RL   [2]
RN   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
KW   Immunoglobulin V region.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; Ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8I4B6559BFC9 CRC64;

Query Match             79.3%;  Score 445;  DB 2;  Length 236;
Best Local Similarity   79.4%;  Pred. No. 5e-38;
  Matches   85;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              |||||||||| ||||||||||| |||| |: : |  ||||||||||| :|||  ::|||
Db         23 DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS 82

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEPPYTFGGGTKVEIK 107
              ||||||||.|:|||||||||||||||||| |   :||:||||||:||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSFPFTFGPGTKVDIK 129
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RESULT 7
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the Bence-
RT   Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
-!-  MISCELLANEOUS: The structure of the V region was determined by
     molecular replacement methods using the known structure of the v
     region of the kappa chain REI.
-!-  MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!-  MISCELLANEOUS: This is a Bence-Jones protein.
DR   PDB; 1JVS; X-ray; A=1-107.
DR   PIR; A91653; KIHUAU.
CC   GO; GO:0005576; C:extracellular; NAS.
CC   GO; GO:0003823; F:antigen binding; NAS.
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DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   STRAND        4      5
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       44     49
FT   STRAND       50     52
FT   TURN         53     54
FT   STRAND       56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       97     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E801187E66F6FB9 CRC64;

Query Match             79.1%;  Score 444;  DB 1;  Length 108;
Best Local Similarity   79.4%;  Pred. No. 2.5e-38;
  Matches   85;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||| |||| |  : |:||||||||||| ::|| :::|.|||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEPPYTFGGGTKVEIK 107
              ||||||||.: |:||||||||| ||||| |||:  .||| |||||||
Db         61 RFSGSGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107
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RESULT 8
ID   Q7TMK3         PRELIMINARY;   PRT;   236 AA.
AC   Q7TMK3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

(Sequence listing — patent document, rotated text, remaining content is BLAST-type alignment results for RESULT 9 KV1V_HUMAN and RESULT 10 KV1P_HUMAN with database annotations.)

RESULT 11
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ID   KV5F_MOUSE     STANDARD;      PRT;   115 AA.
AC   P01638;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region L6 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
DR   PIR; A01921; KVMSL6.
DR   HSSP; P01607; 1BWW.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21   >115       Ig kappa chain V-V region L6.
FT   DOMAIN       21   >115       Framework-1.
FT   DOMAIN       44     54       Complementarity-determining-1.
FT   DOMAIN       55     69       Framework-2.
FT   DOMAIN       70     76       Complementarity-determining-2.
FT   DOMAIN       77    108       Framework-3.
FT   DOMAIN      109   >115       Complementarity-determining-3.
FT   NON_TER     115
FT   DISULFID     43    108       By similarity.
SQ   SEQUENCE  115 AA;  12986 MW;  BA852C58F328B1C3 CRC64;
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Query Match 78.8%; Score 442; DB 1; Length 115;
Best Local Similarity 77.6%; Pred. No. 4.1e-38;
Matches 83; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

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Qy    1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         |||||||||||||||||||||| :|||||:| :||:|||||||||| ||| ||  |:|||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||:|||:| ||||||||||| ||||| | ||:  ||||||||| |
Db   61 RFSGTGSGTDFTLTISSLQPEDIATYYCCQQFDNLPLTFGGGTKVDFK 107
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ID   KV1R_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT   in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC       against 3,4-Pyruvylated galactose and isolated from a patient with
CC       Waldenstrom's macroglobulinemia.
DR   PIR; A01876; KIHUWE.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Monoclonal antibody.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108
SQ   SEQUENCE  108 AA;  11840 MW;  9249B61F0945618C CRC64;
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Query Match 78.6%; Score 441; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 5.2e-38;
Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

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Qy    1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||||||||||||||||||||||| |||  : : |||:|||| ||| |||| |:| |||||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVPS 60

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
         ||||||||:| |||| ||||||||||||||| : | ||| ||||| |
Db   61 RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEVK 107
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RESULT 13
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ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
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Query Match 78.8%; Score 442; DB 1; Length 115;
Best Local Similarity 87.4%; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Matches 83;

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Qy    1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
         ||:||||||| ||| |:||||||||||||||||||||: |:|||||||||||||||||||
Db   21 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKGKSPKTLIYRANRLVDGVPS 80

Qy   61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDFP 95
         |||||||||||:|||||| | ||  |||||||||
Db   81 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDFP 115
```

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RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91663; KIHURE.
DR   PDB; 1AR2; X-ray; @=1-107.
DR   PDB; 1BWW; X-ray; A/B=1-107.
DR   PDB; 1REI; X-ray; A/B=1-107.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   STRAND       60     61
FT   TURN         62     67
FT   STRAND       68     69
FT   TURN         70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       97     98
FT   NON_TER     102    106
FT   STRAND      102    106
FT   SEQUENCE    108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143B1888BC82A CRC64;
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Query Match             78.3%;  Score 439;  DB 1;  Length 108;
Best Local Similarity   79.2%;  Pred. No. 8.4e-38;
Matches   84;  Conservative   6;  Mismatches  16;  Indels   0;  Gaps   0;

Qy      1  DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60
           ||||||||||||||||||||:|||||:|||:||:|:|||||||||||||||:||||||||
Db      1  DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS  60

Qy     61  RFSGSGSGGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEI  106
           |||||||| :|||:||||||||||||||||||:|||| ||||||| |:|
Db     61  RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI  106
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ID   Q6GMX9                  PRELIMINARY;      PRT;     236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073763; AAH73763.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25924 MW;  FDB2093DC560CFF7 CRC64;
```

```
Query Match             77.9%;  Score 437;  DB 2;  Length 236;
Best Local Similarity   76.6%;  Pred. No. 3.4e-37;
Matches   82;  Conservative  13;  Mismatches  12;  Indels   0;  Gaps   0;

Qy      1  DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60
           ||||||||||||||||||||:|||||:|||:||:|:||||:||| || ||||:||||||||
Db     23  DIQMTQSPSSLSASVGHRVTITCRASQNVSRWLAWYQQRPEKAPKSLIYATSSLHSGVPS  82

Qy     61  RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK  107
           |||||||| :|||:|||||||||||||||| |||| ||||||||:||
Db     83  RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGGTKVEIK  129
```

```
Q96SA9
```

```
ID   Q96SA9                    PRELIMINARY;      PRT;    107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96396; AAB68785.1; -.
DR   PIR; B49047; B49047.
DR   PIR; PH0867; PH0867.
DR   PIR; S16840; S16840.
DR   PIR; S31977; S31977.
DR   PIR; S34083; S34083.
DR   PIR; S34086; S34086.
DR   HSSP; P01607; 1BWW.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11520 MW;  4BB43B9C5B577F16 CRC64;
```

```
Query Match             77.8%;  Score 436.5; DB 2;  Length 107;
Best Local Similarity   81.3%;  Pred. No. 1.5e-37;
Matches   87;  Conservative   6;  Mismatches  13;  Indels   1;  Gaps   1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS 60
              |||||||||||||||||| ||::|||||::|| |||||||||||||:||| |:|||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy         61 RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
              ||||||||| :|||||||||||||||||||::|| |||||||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDFATYYC-QQSYSTLTFGGGTKVEIK 106
```

OM protein - protein search, using sw model

GenCore version 5.1.6

Run on: December 29, 2004, 17:46:45 ; Search time 16.323 seconds
                                           (without alignments)
                                           701.451 Million cell updates/sec

Title:
Perfect Score: 642
Sequence: 1 EVQLVQSGAEVKKPGASVKI..........GNFPYYFDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_79:*
        1: pir1:*
        2: pir2:*
        3: pir3:*
        4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	467.5	72.8	137	2	H32513	Ig heavy chain precur
2	459.5	71.6	118	2	S36265	Ig heavy chain v r
3	459.5	71.6	119	2	F30502	Ig heavy chain v r
4	457.5	71.6	128	2	PH0952	Ig heavy chain v r
5	456.5	71.1	150	2	PN0444	Ig heavy chain v r
6	450	70.1	142	2	A32483	Ig heavy chain v r
7	448.5	69.9	120	2	PH0962	Ig heavy chain v r
8	448.5	69.9	128	2	I37267	Ig heavy chain v r
9	448.5	69.9	139	2	A27609	Ig heavy chain v r
10	446	69.5	128	2	C37267	Ig heavy chain v r
11	446	69.5	123	2	D33548	Ig heavy chain v-1
12	445.5	69.4	123	2	S38717	Ig heavy chain v r
13	445	69.3	119	2	S20640	Ig heavy chain v r
14	443.5	69.1	116	2	PH0959	Ig heavy chain v r
15	443	69.0	117	2	S03305	Ig heavy chain v r
16	443	69.0	121	2	H37266	Ig heavy chain v r
17	442.5	68.9	124	2	S19665	Ig heavy chain v r
18	442.5	68.9	135	2	S49530	Ig heavy chain v r
19	441.5	68.8	117	2	S25176	Ig heavy chain v r
20	440	68.8	121	2	F37266	Ig heavy chain v r
21	439	68.5	121	2	PL0200	Ig heavy chain v r
22	439	68.4	122	2	S36271	anti-DNA autoantib
23	438.5	68.3	120	2	S31394	anti-Sm antibody v-
24	438	68.2	118	2	S38565	Ig heavy chain v r
25	438	68.2	119	2	PH0961	Ig heavy chain v r
26	437.5	68.1	120	2	B22769	Ig heavy chain v r
27	437	68.1	125	2	PH0957	Ig heavy chain v r
28	436	67.9	129	2	S46393	Ig heavy chain v r
29	436	67.9	133	2	C33548	Ig heavy chain V-1
30	436	67.9	136	2	S14683	Ig mu chain precur
31	435.5	67.8	131	2	S66537	Ig heavy chain v r
32	435.5	67.8	132	2	PH0954	Ig heavy chain v r
33	435.5	67.8	127	2	PH0955	Ig heavy chain v r
34	435	67.8	129	2	S36260	Ig heavy chain v r
35	435	67.8	129	2	A33548	Ig heavy chain V-1
36	434.5	67.7	116	2	S53751	Ig heavy chain v r
37	434.5	67.7	122	2	S53751	Ig heavy chain v r
38	433.5	67.5	136	2	S31600	Ig heavy chain pre
39	433.5	67.5	139	2	PH0958	Ig heavy chain v r
40	433.5	67.5	287	2	MRMS18	Ig heavy chain pre
41	432.5	67.4	126	2	PC4402	antibody Fab Jel 1
42	432.5	67.4	128	2	B33548	Ig heavy chain V-1
43	432.5	67.4	171	2	A37267	pelB leader/Ig hea
44	431	67.1	127	2	S23623	Ig heavy chain pre
45	431	67.1	160	2	PL0105	anti-PR2 erythrocy

ALIGNMENTS

RESULT 1
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.,
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: GB:M20831; NID:gi196949; PIDN:AAA38848.1; PID:gi196950
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   72.8%; Score 467.5; DB 2; Length 137;
Best Local Similarity 73.9%; Pred. No. 8.3e-35;
Matches 88; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYGDPGY 60
          :|| |||||||||||||:||| :|||||||||:|::||:||:||||||| ||:||
Db   20 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYGGSTSY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYYFDYWGQGTLVTVSS 119
         :|||||||||||||| ||||||:||||:||||||: ||| ||||||||||||||||
Db   80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARK-NYGSSFDYWGQGTTLTVSS 137
```

RESULT 2
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display librarie
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:g331121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   71.6%; Score 459.5; DB 2; Length 118;
Best Local Similarity 73.9%; Pred. No. 3.7e-34;

RESULT 3
F30502
Ig heavy chain V region (A52) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: F30502
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-119 <EIL>
C;Superfamily: immunoglobulin; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 457.5; DB 2; Length 128;
Best Local Similarity 72.1%; Pred. No. 3.7e-34;
Matches 88; Conservative 11; Mismatches 19; Indels 1; Gaps 1;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        |:|| |:||||||||||||||||:|||:|:|| | :||||||||||||||:||||||||
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPFYYFDYWGQGTLVTVSS 119
        |||| |||||:|||||||||||||||||||||||||||  | |||||||||||||||
Db   61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCA-RDFLSGYLDYWGQGTLVTVSS 118
```

RESULT 4
PH0952
Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0952
A;Molecule type: nucleic acid sequence not shown
A;Residues: 1-128 <MAR>
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin V region; immunoglobulin homology
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-116/Region: complementarity-determining 3

Query Match 71.3%; Score 457.5; DB 2; Length 128;
Best Local Similarity 68.0%; Pred. No. 6e-34;
Matches 87; Conservative 15; Mismatches 17; Indels 9; Gaps 1;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        |||||||||||:||||||||||:|||:|:| :||||||||||||||:||||||||
Db    1 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGKINPYYGSTSY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCA----RRGNPFYYFDYWGQGTLVT 116
        ||||||:||||||||:|||||:| |||||:|||||||    ||||   | |||||||||:
Db   61 NQKFKGQATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGRLRRGG---YFDYWGQGTTLT 117

Qy  117 VSS 119
            |||
Db  118 -VSS 119
```

RESULT 5
PN0444
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymer
A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0444
A;Molecule type: mRNA
A;Residues: 1-150 <KAL>
A;Cross-references: GB:L02346
C;Superfamily: immunoglobulin V region; immunoglobulin; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-150/Product: Ig heavy chain V region #status predicted <MAT>
F;20-117/Domain: variable region <VRG>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 456.5; DB 2; Length 150;
Best Local Similarity 74.8%; Pred. No. 8.7e-34;
Matches 89; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        ||||:||||||:||||:||||||:|||:|:| :||||||||||||||:||:
Db   20 EVQLQQSGAELVKPGTSVKISCKASGYIFTDYNMDWVKQSHGKSLEWIGDIDPNFDSSSY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPFYYFDYWGQGTLVTVSS 119
        |||||||||||||||:||||||| || |||:|||:||||||
Db   80 NQKFKGKATLTVDKSSNTAYMELRSLTSEDSAVYMCARGGNYDYIWGSYRSNDAFDIWGQ 137
```

RESULT 6
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi
A;Reference number: A32483; MUID:89273586; PMID:2499327
A;Accession: A32483
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin V region; immunoglobulin homology

Query Match 70.1%; Score 450; DB 2; Length 142;
Best Local Similarity 69.3%; Pred. No. 3.1e-33;
Matches 88; Conservative 10; Mismatches 21; Indels 8; Gaps 1;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        ||||||||||||||||||||||||||||||||||||
Db    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
```

```
Db      11  QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPQGLEWMGIINPSGNSTNY  70

Qy      61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYF---------DYWGQG 112
            ||||| |||:||||||||||  : :|||:|||                       |||||
Db      71  AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130

Qy     113  TLVTVSS  119
            ||||||
Db     131  TLVTVSS  137
```

RESULT 7

PH0962

Ig heavy chain V region (G6+ T-L42) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0962
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0962
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-120 <MAR>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keyword: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-108/Region: complementarity-determining 3

Query Match   69.9%; Score 448.5; DB 2; Length 120;
Best Local Similarity   71.9%; Pred. No. 3.6e-33;
Matches 87; Conservative 15; Mismatches 16; Indels 3; Gaps 2;

```
Qy       1  EVQLVQSGGAEVKKPGASVKVSCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY  60
            ||||||| |||:|||||||||  :||||::||||:| |||||| ||||||:||||| :
Db       1  QVQLVQSGAEVKKPGSSVKVSCKASGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY   60

Qy      61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRG--NFPYYFDYWGQGTLVTVS  118
            |||||||||||||||||||||||||||||||||:|||||   :||| |||||||||||||
Db      61  AQKFQGRVTIADESTSTAYMELSSLRSEDTAVYYCARGGVAGRP-HFDYWGQGTLVTVS   119

Qy     119  S  119
            |
Db     120  S  120
```

RESULT 8

I37267

Ig heavy chain V region (I29) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: I37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: I37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keyword: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match   69.9%; Score 448.5; DB 2; Length 128;
Best Local Similarity   71.5%; Pred. No. 3.8e-33;
Matches 88; Conservative   9; Mismatches 21; Indels 5; Gaps 1;

```
Db      62  QXFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG  116

Qy     113  TLVTVSS  119
            ||||||
Db     131  TLVTVSS  137
```

RESULT 9

A27609

Ig heavy chain precursor V region (I29) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
C;Genetics:
A;Introns: 16/1
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Product: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   69.9%; Score 448.5; DB 2; Length 139;
Best Local Similarity   71.7%; Pred. No. 4.2e-33;
Matches 86; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

```
Qy       2  VQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGYS  61
            |||||| |||:||||||||| :||||::||||:||||||| |||||||:|||||: :
Db       6  VQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGTSYN   65

Qy      61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRG------NFPYYFDYWGQGTLVTVS  118
            |||||  :|||||||||||||||| :|||:||||||||||      :||||  |||||||||||
Db      66  QKFKGKATLTVDKSSTAYMELRSLTSEDSAVYYCARRGLTTVVAKSYYFDVWGTGTTLT  125

Qy     119  S  119
            |
Db     126  VSS  128
```

RESULT 10

C37267

Ig heavy chain V region (Py69) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: C37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of ant
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: C37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match   69.5%; Score 446.5; DB 2; Length 128;
Best Local Similarity   69.9%; Pred. No. 5.8e-33;
Matches 86; Conservative 11; Mismatches 21; Indels 5; Gaps 1;

```
Qy       1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY  60
            |||||||||||:|||||||| :||||::||||:||||||| ||||||:||| ||| :
Db      20  EVQLQQSGPELVKPGASVKMSCKASGYTFTDYVMHWVKQSNGKSLEWIGYINPYNDYTSY  79

Qy      61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYY-FDYWGQGTLVTVSS  119
            ||||||||||||||:|:|| : ||||:|||:||||||||||:::|  |||||||||||||
Db      80  NQKFKGKATLTVDKSSTAYMQLNSLTSEDSAVYYCARYSYSYSYAMDYWGQGTSVTVSS  139
```

```
Qy       2  VQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGYS  61
            |||||||||||||||||||||: ||||::||||:||||||| |||||||:||||: :
```

```
Db      6  VQLQQSGPELVKPGASMKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGRFNPNSGGSTYN  65

Qy     62  QKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNF------PYYFDYWGQGTLVT  116
           ||||||||||||||||||||||||||||||||||||||||      ||:||||||||||||
Db     66  QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGPYGNYYTSYYFDYWGQGTLLT  125

Qy    117  VSS 119
           |||
Db    126  VSS 128
```

```
RESULT 11
D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575; PMID:2503826
A;Accession: D33548
A;Molecule type: mRNA
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match             69.5%;  Score 446;  DB 2;  Length 123;
Best Local Similarity   67.5%;  Pred. No. 6.2e-33;
Matches   83;  Conservative   18;  Mismatches   18;  Indels   4;  Gaps   1;

Qy      1  EVQLVQSGAEVKKPGASVKISCKVSGYTVSSCEASGYTFTGHYMHWVRQAPGKGLEWMGWINPNSGGTNY  60
           :||||||||||||||||||||||||||:              :||||||||||||:||:||:||:|:||:
Db      1  QVQLVQSGAEVKKPGASVKVSCEASGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNY  60

Qy     61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRG----NPFYYFDYWGQGTLVT  116
           |||||||||||||||:||||||||||:||||||||||||    :||||||||||||||||
Db     61  AEKFQGRVTITRDTSINTAYMELSRLRSDDTAVYYCARASYCGYDCYYFPDYWGQGTLVT  120
```

```
Db     63  KFKGKATLTVDKSSSTAYMELSSLTSEDSAVYYCARENGNF--YFDYWGQGTLLTVSS  118
```

```
RESULT 12
S38717
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38717
R;Cimanis, A.Y.
A;Reference number: S38717
submitted to the EMBL Data Library, November 1993
A;Accession: S38713
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-118 <CIM>
A;Cross-references: EMBL:X76020; NID:g416099; PIDN:CAA53607.1; PID:g1334262
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match             69.4%;  Score 445.5;  DB 2;  Length 118;
Best Local Similarity   72.9%;  Pred. No. 6.5e-33;
Matches   86;  Conservative   11;  Mismatches   18;  Indels   3;  Gaps   2;

Qy      3  QLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGYSQ  62
           ||||:||||||||:|:|||||::||||||:||:|||||||||||||||||||||||||:|
Db      3  QLQQSGPDLVKPGASVKMSCKASGYTFNYVIHWVKQRPGQGLEWIGYIHPYNDGSKYND  62

Qy     63  KFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAR-RGNFPYYFDYWGQGTLVTVSS  119
```

```
Db     63  KFKGKATLTVDKSSSTAYMELSSLTSEDSAVYYCARRGNGNF--YFDYWGQGTLLTVSS  118
```

```
RESULT 13
S20640
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20640; S20644
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20640
A;Accession: S20640
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-119 <LOS>
A;Cross-references: EMBL:X65002; NID:g52600; PIDN:CAA46135.1; PID:g52601; EMBL:X64999; 
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match             69.3%;  Score 445;  DB 2;  Length 119;
Best Local Similarity   70.6%;  Pred. No. 7.3e-33;
Matches   84;  Conservative   14;  Mismatches   21;  Indels   0;  Gaps   0;

Qy      1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY  60
           :||||||||||||||:||||||:|:|||||:||:|||||||||:|:|||||||||||||:
Db      1  EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVIHWVKQKPGRGLEWIGYINPYNDGSKY  60

Qy     61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYYFDYWGQGTLVTVSS  119
           :|||||||||||||:|||||||:||||||||||||||||:  :||||||||||||||||
Db     61  NEMFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARRATKGSWFAYWGQGTLVTVSA  119
```

```
RESULT 14
PH0959
Ig heavy chain V region (G6+ T-L26) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0959
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0959; MUID:92202880; PMID:1552291
A;Accession: PH0952; MUID:92202880; PMID:1552291
A;Molecule type: DNA
A;Residues: 1-116 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin; immunoglobulin homology
A;Status: nucleic acid sequence not shown
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-104/Region: complementarity-determining 3

Query Match             69.1%;  Score 443.5;  DB 2;  Length 116;
Best Local Similarity   71.4%;  Pred. No. 9.7e-33;
Matches   85;  Conservative   15;  Mismatches   16;  Indels   3;  Gaps   1;

Qy      1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY  60
           :||||||||||||||:||||||:|:|||||:||:|||||||||:|:|||||||||||||
Db      1  QVQLVQSGAEVKKPGASVKMSCKASGYTFTSYAISWVRQAPGQGLEWMGGIIPIFGTANY  60

Qy     61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARGN-----NPFYYFDYWGQGTLVTVSS  119
           :|||||||||||||:||||||||||:||||:||||||||     ||:|||||||||||||||||
Db     61  AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGDN---WFDPWGQGTLVTVSS  116
```

RESULT 15

S03305

Ig heavy chain V region (6B12) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: JL0044; S05276; S03305
R;Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A;Title: Do antibodies recognize amino acid side chains of protein antigens independent1
A;Reference number: JL0043; MUID:88258372; PMID:2455014
A;Accession: JL0044
A;Molecule type: mRNA
A;Residues: 1-117 <VAN>
A;Cross-references: EMBL:X12381
R;Metzger, D.W.
submitted to the EMBL Data Library, July 1988
A;Reference number: S05276
A;Accession: S05276
A;Molecule type: mRNA
A;Residues: 1-116, 'T' <MET>
A;Cross-references: EMBL:X12381; NID:g52094; PIDN:CAA30939.1; PID:g9301170
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   69.0%; Score 443; DB 2; Length 117;
Best Local Similarity   72.3%; Pred. No. 1.1e-32;
Matches   86; Conservative   10; Mismatches   21; Indels   2; Gaps   1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYGDPGY   60
           |||.||||||.|||||||||:|||.|||||||:|: |:|.: |||||||||||:|| |
Db   1 EVQLQQSGPEAGKPGASVKMSCKASGYTFTDYYINWVKQSHGKSLEWIGYIYPNIDETAY   60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS   119
           |||||||||||||||:|||||||||:||||||||.||: ||||| |:||||:||||||
Db   61 SQKFKGKATLTVDKSSSTAYMELRSLTSDDSAVYYCARRNN--VYFDYWGQGTTLTVSS   117

Search completed: December 29, 2004, 18:06:58
Job time : 17.4897 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 ; Search time 82.1416 seconds
(without alignments)
833.556 Million cell updates/sec

Title:
Perfect Score: 642
Sequence: 1 EVQLVQSGAEVKKPGASVKI............GNFPYYFDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	468	72.9	120	2	Q920E8	Q920e8 mus musculu
2	454	70.7	119	2	Q9UL94	Q9ul94 homo sapien
3	450.5	70.7	124	2	Q9UL92	Q9ul92 homo sapien
4	449	69.9	464	2	Aah19337	Aah19337 homo sapi
5	448.5	69.9	498	2	Q6N041	Q6n041 homo sapien
6	448.5	69.9	498	2	Cae45829	Cae45829 homo sapi
7	445	69.3	123	2	Q8VIJ1	Q8vij1 mus musculu
8	445	69.3	146	2	Q24r8	Q24r8 mus musculu
9	441.5	68.8	465	2	06pjb2	06pjb2 mus musculu
10	441.5	68.8	465	2	Aah18280	Aah18280 mus muscu
11	440	68.5	470	2	Q7tmk1	Q7tmk1 mus musculu
12	439	68.4	119	2	Q9gyz2	Q9gyz2 schistosoma
13	439	68.4	472	2	06pja7	06pja7 mus musculu
14	439	68.4	472	2	Aah18535	Aah18535 mus muscu
15	438	68.2	117	2	Q9qxf0	Q9qxf0 mus musculu
16	438	68.2	470	2	Aah62336	Aah62336 homo sapi
17	433.5	67.5	139	1	P01751	P01751 mus musculu
18	433.5	67.5	145	2	Q24q7	Q24q7 mus musculu
19	433	67.4	144	2	Q24p5	Q24p5 mus musculu
20	432.5	67.4	145	2	Q24r4	Q24r4 mus musculu
21	431.5	67.2	467	2	Aah37361	Aah37361 homo sapi
22	431.5	67.1	145	2	Q24q6	Q24q6 mus musculu
23	430.5	67.1	145	2	Q24r1	Q24r1 mus musculu
24	430.5	66.9	159	2	Q96qs0	Q96qs0 homo sapien
25	429.5	66.9	145	2	Q24q9	Q24q9 mus musculu
26	429.5	66.9	482	2	Q8k172	Q8k172 mus musculu
27	429	66.8	473	2	Q9d8l4	Q9d8l4 mus musculu
28	428.5	66.7	116	2	Q9d8l4	Q9dl89 homo sapien
29	428.5	66.7	145	2	Q24p7	Q24p7 mus musculu
30	428	66.7	117	1	HV12 MOUSE	P01756 mus musculu
31	426.5	66.4	143	2	Q924R0	Q924r0 mus musculu
32	426.5	66.4	143	2	Q924R7	Q924r7 mus musculu
33	426.5	66.4	145	2	Q924R3	Q924r3 mus musculu
34	426.5	66.4	481	2	Q8VCV5	Q8vcv5 mus musculu
35	426.5	66.4	518	2	Q6N030	Q6n030 homo sapien
36	426.5	66.4	518	2	Cae45841	Cae45841 homo sapi
37	426	66.4	125	2	Q9UL95	Q9ul95 homo sapien
38	426	66.4	142	2	Q92401	Q92401 mus musculu
39	425	66.2	146	2	Q92403	Q92403 mus musculu
40	424.5	66.1	109	2	Q9L75	Q9l75 mus musculu
41	424.5	66.0	473	2	Q99125	Q99125 mus musculu
42	424	66.0	140	2	Q924R2	Q924r2 mus musculu
43	423.5	66.0	143	2	Q924Q5	Q24q5 mus musculu
44	423	65.9	117	2	Q9QXE9	Q9qxe9 mus musculu
45	423	65.9	614	2	Q7TMT6	Q7tmt6 mus musculu

ALIGNMENTS

RESULT 1
ID   Q920E8
AC   Q920E8;   PRELIMINARY;   PRT;   120 AA.
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Pterin-mimicking anti-idiotope heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307936; AAL09420.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
NON_TER   1
NON_TER   120
SQ   SEQUENCE   120 AA;   13204 MW;   DC4834AB1DE56F3C CRC64;

Query Match   72.9%; Score 468; DB 2; Length 120;
Best Local Similarity   75.0%; Pred. No. 1.8e-40;
Matches   90; Conservative 10; Mismatches 18; Indels 2; Gaps 1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              :||||||:||||||||||||||:|||:||::||| ||.|:|||||||:|||||||| :
Db   1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNGKSLEWIGNIDPYYGGTSY 60

Qy   61 SQKFKGKRATLTVDKSSTAYMELSSLRSEDTAVYYCA--RRGNFPYYFDYWGQGTLVTVS 118
              : |||| ||||||||||| ||||||| ||||||||| ||||||||||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCAVIYYGNSPAWFAYWGQGTLVTVS 120

RESULT 2
ID   Q9UL94
AC   Q9UL94;   PRELIMINARY;   PRT;   119 AA.
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;

```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035020; AAD56256.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13205 MW;  13E64F53454P4A16E CRC64;

Query Match             70.7%;  Score 454;  DB 2;  Length 119;
Best Local Similarity   72.3%;  Pred. No. 5e-39;
Matches   86;  Conservative   12;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMWVRQAPGKGLEWIGYIDPYYGDPGY 60
              |||||:|||||||||||||:||| |:|:||||:|||:|||||||||:|:||:|
Db          1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSWTTNY 60

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARGNFPYYFDYWGQGTLVTVSS 119
              ||:|:|||:|| ||||||||||||||||||||||||||
Db         61 AQKFQGKVTMTRDTSISTVYMELSRLRSDDTAVYYCARGGGRGLWFDPWGQGTLVTVSS 119


RESULT 3
ID   Q9UL92      PRELIMINARY;      PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035022; AAD56258.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;

Query Match             70.4%;  Score 450.5;  DB 2;  Length 124;
Best Local Similarity   70.4%;  Pred. No. 1.2e-38;
Matches   88;  Conservative   13;  Mismatches   17;  Indels    7;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMWVRQAPGKGLEWIGYIDPYYGDPGY 60
              |||||:|||||||||||||:||| |:|:||||:|||:|||||||||:|:||:|
Db          1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARGNFPYY----FDYWGQGTL 114
              ||:|:|||:|| ||||||||||:|||||:|:||||||||:|     |:|||||||
Db         61 AQKFQGRVTMTRDTSISTVYMELSSLRSEDTAVYYCA-RGLYVVVPAAFSRFDYWGQGTL 119

Qy        115 VTVSS 119
              |||||
Db        120 VTVSS 124


RESULT 4
ID   AAH19337    PRELIMINARY;      PRT;   464 AA.
AC   AAH19337;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019337; AAH19337.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   464 AA;  50891 MW;  2F80673E74E2A485 CRC64;

Query Match             69.9%;  Score 449;  DB 2;  Length 464;
Best Local Similarity   72.3%;  Pred. No. 7.7e-38;
Matches   86;  Conservative   11;  Mismatches   18;  Indels    4;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMWVRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||:||| |:|:||||:|||:|||||||||:|:||:|
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSGGSTY 79

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARGNFPYYFDYWGQGTLVTVSS 119
              :||:|:|||:|| |||||||||:|||||||||||||||||:|     |||||||||||
Db         80 AQNFQGRVTMTRDTSTSTVYMELTSLRSEDTAVYYCARIG----VHDYWGQGTQVTVSS 134


RESULT 5
ID   Q6N041      PRELIMINARY;      PRT;   498 AA.
AC   Q6N041;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

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DB   Hypothetical protein DKFZp686O16217 (Fragment).
GN   Name=DKFZp686O16217;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   THE GERMAN HUMAN cDNA CONSORTIUM;
RA   Pouska A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640710; CAE45829.1; -.
DR   InterPro; IPR000599; IG.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003597; IG_c1.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
FT   NON_TER        1
SQ   SEQUENCE   498 AA;  54125 MW;  40B3208A84E03B46 CRC64;

Query Match     69.9%;  Score 448.5;  DB 2;  Length 498;
Best Local Similarity   67.7%;  Pred. No. 9.4e-38;
Matches   84;  Conservative  17;  Mismatches  18;  Indels   5;  Gaps   1;

Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
          :||||||||| ||||||||||:| |:|:|| : ||||||||| | :|| ::|: :||||
Db    1 QVQLVQSGADVKKPGASVKVSCKASGYTFTNYFFHWVRQAPGQGPEWMGMINPRDGSTKY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRG-----NPYYFDYWGQGTLV 115
          :|||| | :| ||:||||| |||||||||||| || ||       | |||||||||||||
Db   95 AQRFQGRVSMTRDTSTSTIYMELSSLRSEDTAMFFCARAGPGYGTSASYYFDYWGQGTLV 154

Qy  116 TVSS 119
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Db  155 TVSS 158
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RESULT 6
CAE45829
ID   CAE45829         PRELIMINARY;      PRT;   498 AA.
AC   CAE45829;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686O16217 (Fragment).
GN   Name=DKFZp686O16217;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Pouska A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA   Mewes H.W., Weil B., Amid C., Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640710; CAE45829.1; -.
DE   Hypothetical protein.
SQ   SEQUENCE   498 AA;  40B3208A84E03B46 CRC64;

Query Match     84;  Conservative  17;  Mismatches  18;  Indels   5;  Gaps   1;

Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
          :||||||||| ||||||||||:| |:|:|| : ||||||||| | :|| ::|: :||||
Db    1 QVQLVQSGADVKKPGASVKVSCKASGYTFTNYFFHWVRQAPGQGPEWMGMINPRDGSTKY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRG-----NPYYFDYWGQGTLV 115
          :|||| | :| ||:||||| |||||||||||| || ||       | |||||||||||||
Db   61 AQRFQGRVSMTRDTSTSTIYMELSSLRSEDTAMFFCARAGPGYGTSASYYFDYWGQGTLV 115

Qy  116 TVSS 119
          ||||
Db  116 TVSS 119
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RESULT 7
Q8VIJ1
ID   Q8VIJ1           PRELIMINARY;      PRT;   123 AA.
AC   Q8VIJ1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-DNA heavy chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H/HeJ-lpr/lpr;
RX   MEDLINE=96409289; PubMed=8814271;
RA   Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT   "Differences in V kappa gene utilization and VH CDR3 sequence among
RT   anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL   Eur. J. Immunol. 26:2225-2233(1996).
DR   EMBL; U59154; AAB02916.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1
FT   NON_TER      123
SQ   SEQUENCE   123 AA;  13806 MW;  CC0037A80689911E CRC64;

Query Match     69.3%;  Score 445.;  DB 2;  Length 123;
Best Local Similarity   68.8%;  Pred. No. 4.4e-38;
Matches   86;  Conservative  14;  Mismatches  17;  Indels   8;  Gaps   2;

Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
          |:|| ||| |:||||||||||||| || : ||||| ||| ||: :||:| |||| || |
Db    1 EIQLQQSGTELVKPGASVKISCKASGYSFTGYNMNWVRQSHGKSLEWVGDINPYYGDPGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRG-----FDYWGQGTL 114
          |||||||||||||||:: :||| :||:||||::||||   |       |||||||
Db   61 SQKFKGKATLTVDKSSRTAYMQLNSLTSEDSAVYYCAR--DYTYYTVDBGCFAYWGDINPYYGDPGY 118

Qy  115 VTVSS 119
          ||||:
Db  119 VTVSA 123
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RESULT 8
Q924R8
ID   Q924R8           PRELIMINARY;      PRT;   146 AA.
AC   Q924R8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
```

RESULT 9

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ID   Q6PJB2      PRELIMINARY;   PRT;   465 AA.
AC   Q6PJB2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067781; BAB63266.1; -.
DR   PIR; F28833; F28833.
DR   PIR; F28833; F28833.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    146    146
SQ   SEQUENCE   146 AA;  16216 MW;  92460F1FDF1B7538 CRC64;

Query Match             69.3%;  Score 445;  DB 2;  Length 146;
Best Local Similarity   70.2%;  Pred. No. 5.3e-38;
Matches   85;  Conservative   14;  Mismatches   20;  Indels    2;  Gaps    1;

Qy    1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMHWVRQAPGKGLEWIGYIDPYYGDPGY  60
         |||||||||||| |||||:|||||||||| ||||||:|||||||| ||||||||||||||
Db    1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY  60

Qy   61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARR--GNFPYYFDYWGQGTLVTVS 118
         :||||:|||||||| :|||| :|||| :|||:||||||    |:|||||||||||:|:|||
Db   61  NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSYYGSSLYYFDYWGQGTTLTVS 120

Qy  119  S 119
         |
Db  121  S 121
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RESULT 10

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ID   AAH18280      PRELIMINARY;   PRT;   465 AA.
AC   AAH18280;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018280; AAH18280.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; Ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51329 MW;  394F43C4EBDB3B21 CRC64;

Query Match             68.8%;  Score 441.5;  DB 2;  Length 465;
Best Local Similarity   70.6%;  Pred. No. 4.6e-37;
Matches   84;  Conservative   12;  Mismatches   20;  Indels    3;  Gaps    1;

Qy    1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMHWVRQAPGKGLEWIGYIDPYYGDPGY  60
         |||| ||||: |||||||:|||||||||| ||||:  :|||||| ||| |||||:|||:||
Db    1  QVQLKQSGAELVKPGASVKLSCKASGYTFTNSYIMHWVKQRPGQGLEWIGYFSPYNDDTKC  60

Qy   61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
         :||||||||||:||:::|||||||||| ||:|||||||    |:||||||||||:|:|||
Db   80  NEKFKGKATLTADKSSSTAYMELSSLTSEDSAVYYCARG---YYVFDYWGQGTITVSS 135
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RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018280; AAH18280.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;

```
Query Match             68.8%;  Score 441.5;  DB 2;  Length 465;
Best Local Similarity   70.6%;
Matches   84;  Conservative   12;  Mismatches   20;  Indels    3;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              |||||||||||||||||||||||: ||||||||||::|||||||||||||||||||||||
Db         20 QVQLQSGGAELVKPGASVKLSCKASGYTFNSYIMHWVKQRPGQGLEWIGYFSPYNDDTKC 79

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              ::|||||||||||||||||| ||||||| ||||||||||   |:||:|||||||||||||
Db         80 NEKFKGKATLTFADKSSSTAYMELSSLTSEDSAVYYCARG---YYVFDYWGQGTTITVSS 135
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RESULT 11
Q7TMK1

ID   Q7TMK1
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RL   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;
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Query Match             68.5%;  Score 440;  DB 2;  Length 470;
Best Local Similarity   70.5%;  Pred. No. 6.7e-37;
Matches   86;  Conservative   13;  Mismatches   19;  Indels    4;  Gaps    2;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||| ||| |||||||||||||:||||||| ||||||||| ||| |||||||||||||||
Db         20 EVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY 79

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAR---RGNFPYYFDYWGQGTLVTV 117
              :||||||||||||||:||||||:||| ||||||||||||   :| |:|||||||||||||
Db         80 NQKFKGKATLTVDKSSSTAYMEINSLTSEDSAVYYCARYYSGSY-WYFDVWGAGTTVTV 138

Qy        118 SS 119
              || 
Db        139 SS 140
```

```
RESULT 12
Q9GYZ2

ID   Q9GYZ2;
AC   Q9GYZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE   (Fragment).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF282622; AAG01452.1; -.
DR   HSSP; P01751; 1A6W.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
NON_TER        1      1
NON_TER      119    119
SQ   SEQUENCE   119 AA;  13567 MW;  BA89387 3FD5FA6AB CRC64;
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RESULT 13

Query Match　　　68.4%;　Score 439;　DB 2;　Length 119;
Best Local Similarity　69.7%;　Pred. No. 1.8e-37;
Matches　83;　Conservative　12;　Mismatches　24;　Indels　0;　Gaps　0;

Qy　　1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
　　　　:|||||||||||||:||||:||||||||||||||||||||||||||:|||||||||||
Db　　1 QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWRQAPGHGLEWIGYINPSRGYTNY 60

Qy　61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPFYYFDYWGQGTTLVTVSS 119
　　　　|||||:|||||||||| |||||||||||||||||:|||| ||||||||||||:||||
Db　61 NQKFKDRVTMTTDKSFSTAYMDLRSLRSADSAVTYCARYYDHYCLDYWGQGTTVVSS 119

ID　Q6PJA7　　　　　PRELIMINARY;　　PRT;　　472 AA.
AC　Q6PJA7;
DT　05-JUL-2004 (TrEMBLrel. 27, Created)
DT　05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT　05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE　Hypothetical protein.
OS　Mus musculus (Mouse).
OC　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC　Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX　NCBI_TaxID=10090;
RN　[1]
RP　SEQUENCE FROM N.A.
RC　STRAIN=Czech II;
RC　TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.;
RX　MEDLINE=22388257; PubMed=12477932;
RA　Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA　Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA　Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA　Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA　Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA　Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA　Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA　Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA　Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA　Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA　Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA　Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA　Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA　Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA　Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA　Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA　Jones S.J., Marra M.A.;
RT　"Generation and initial analysis of more than 15,000 full-length human
RT　and mouse cDNA sequences.";
RL　Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR　EMBL; BC018535; AAH18535.1; -.
DR　InterPro; IPR003599; Ig.
DR　InterPro; IPR007110; Ig-like.
DR　InterPro; IPR003597; Ig_c1.
DR　InterPro; IPR003006; Ig_MHC.
DR　InterPro; IPR003596; Ig_v.
DR　Pfam; PF07654; C1-set; 3.
DR　Pfam; PF00047; Ig; 4.
DR　SMART; SM00409; IG; 2.
DR　SMART; SM00407; IGc1; 3.
DR　SMART; SM00406; IGv; 1.
DR　SMART; SM00408; IG_like; 4.
DR　PROSITE; PS50835; IG_LIKE; 4.
DR　PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW　Hypothetical protein.

SQ　SEQUENCE　472 AA;　52299 MW;　165169C23D55D4AB CRC64;

Qy　117 VSS 119
　　　　|||
Db　140 VSS 142

RESULT 14

Query Match　　　68.4%;　Score 439;　DB 2;　Length 472;
Best Local Similarity　69.1%;　Pred. No. 8.5e-37;
Matches　85;　Conservative　14;　Mismatches　20;　Indels　4;　Gaps　1;

Qy　　1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
　　　　:|||||||||||||:||||:|||||||||||||||||| :||||||||||||||||||||
Db　20 EVQLQQSGPELVKTGASVKMSCKASGYTFSDYYMHWVKQSHGKSLEWIGYIYPNNGGNGY 79

Qy　61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAR----RGNPFYYFDYWGQGTTLVT 116
　　　　|||||||||||:|||:||||||||||||||||||||| ||||||||||||||||| |
Db　80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGVISYSYSYDHYPFDYWGQGTTIT 139

ID　AAH18535　　　　PRELIMINARY;　　PRT;　　472 AA.
AC　AAH18535;
DT　02-MAR-2004 (TrEMBLrel. 27, Created)
DT　02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT　02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE　Hypothetical protein.
OS　Mus musculus (Mouse).
OC　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC　Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX　NCBI_TaxID=10090;
RN　[1]
RP　SEQUENCE FROM N.A.
RC　STRAIN=Czech II; TISSUE=Mammary tumor;
RX　MEDLINE=22388257; PubMed=12477932;
RA　Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA　Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA　Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA　Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA　Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA　Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA　Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA　Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA　Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA　Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA　Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA　Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA　Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA　Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA　Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA　Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA　Jones S.J., Marra M.A.;
RT　"Generation and initial analysis of more than 15,000 full-length human
RT　and mouse cDNA sequences.";
RL　Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR　EMBL; BC018535; AAH18535.1; -.
KW　Hypothetical protein.
SQ　SEQUENCE　472 AA;　52299 MW;　165169C23D55D4AB CRC64;

Qy　61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAR----RGNPFYYFDYWGQGTTLVT 116

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Db      80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGYISYYSYDHYFDYWGQGTTIT 139
           :|||||||||||||||||||||||||||||||||||||||   :: :||||||| :|
Qy     117 VSS 119
           |||
Db     140 VSS 142

RESULT 15
Q9QXF0
ID   Q9QXF0          PRELIMINARY;      PRT;    117 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   PIR; PH0973; PH0973.
HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     117     117
SQ   SEQUENCE   117 AA;  13060 MW;  D816AD0858A47E4C CRC64;

Query Match             68.2%;  Score 438;  DB 2;  Length 117;
Best Local Similarity   71.4%;  Pred. No. 2.2e-37;
Matches   85;  Conservative 13;  Mismatches 19;  Indels  2;  Gaps  1;

Qy      1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
          |||| |||:|| |:||||||||||| ||||:|:|| |:||:|||||||||||:|:
Db      1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy     61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPFYFDYWGQGTLVTVSS 119
          :||||||||||||||:|||||:|:|| |||||||||||    :|||||||||||:|||
Db     61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DKDYYFDYWGQGTTLTVSS 117
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OM protein - protein search, using sw model.

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GenCore version 5.1.6

Run on: December 29, 2004, 17:37:57 ; Search time 81.7906 Seconds
(without alignments)
521.928 Million cell updates/sec

Title:
Perfect score: 642
Sequence: 1 EVQLVQSGAEVKKPGASVKI...........GNFPYYFDYWGQGTLVTVSS 119

Scoring table:
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	530	82.6	117	2	Aaw84097	Aaw84097 Humanised
2	504.5	78.6	588	2	Aaw71880	Aaw71880 Anti-huma
3	504.5	78.6	588	3	Aab12917	Aab12917 Anti-huma
4	504	78.5	117	8	Adl11892	Adl11892 CDR_trans
5	504	78.5	136	4	Aay77596	Aay77596 Anti-huma
6	504	78.5	136	4	Aab78865	Aab78865 Anti-huma
7	503	78.3	110	2	Aaw84099	Aaw84099 Vitronect
8	497.5	77.5	135	2	Aar29017	Aar29017 pUC-RVh-1
9	496.5	77.3	116	2	Aaw22418	Aaw22418 Reshaped
10	496.5	77.3	135	2	Aar29016	Aar29016 pUC-RVh-1
11	492.5	76.7	144	2	Aaw73187	Aaw73187 Fragment
12	492	76.6	117	8	Adl11893	Adl11893 CDR_trans
13	492	76.6	136	3	Aay77600	Aay77600 Anti-huma
14	492	76.6	136	4	Aab78869	Aab78869 Anti-huma
15	490.5	76.4	135	3	Aab07965	Aab07965 A heavy c
16	490.5	76.4	588	2	Aaw71881	Aaw71881 Anti-huma
17	490.5	76.4	588	3	Aab12918	Aab12918 Anti-huma
18	488.5	76.1	116	2	Aar25726	Aar25726 Humanised
19	488.5	76.1	116	4	Aab69686	Aab69686 Human Eu
20	488.5	76.1	116	4	Aab69672	Aab69672 Humanised
21	488.5	76.1	116	8	Ado47777	Ado47777 Humanised
22	488.5	76.1	116	8	Ado47719	Ado47719 Humanised
23	487	75.9	117	6	Abr42726	Abr42726 Anti-tiss
24	486.5	75.8	118	5	Adg24496	Adg24496 Humanised
25	486.5	75.8	135	3	Aay80289	Aay80289 Humanised
26	486.5	75.8	144	2	Aaw73172	Aaw73172 Heavy cha
27	486.5	75.8	144	2	Aaw73189	Aaw73189 Fragment
28	486.5	75.8	144	2	Aay28374	Aay28374 Human hea
29	486	75.7	117	6	Abr42728	Abr42728 Anti-tiss
30	484.5	75.5	144	2	Aaw73188	Aaw73188 Fragment
31	483.5	75.3	116	2	Aaw58514	Aaw58514 Protein S
32	483.5	75.3	116	2	Aaw37812	Aaw37812 Humanised
33	483.5	75.3	116	4	Aab69645	Aab69645 Humanised
34	483.5	75.3	116	6	Adl01227	Adl01227 Murine an
35	483.5	75.3	122	6	Aao27203	Aao27203 Chimeric
36	483.5	75.3	135	2	Aar24107	Aar24107 Humanised
37	483.5	75.3	135	2	Aar06369	Aar06369 Anti-Tac
38	483.5	75.3	135	3	Aay80291	Aay80291 Humanised
39	483.5	75.3	135	3	Aay80288	Aay80288 Humanised
40	483.5	75.3	135	4	Aab69653	Aab69653 Humanised
41	483.5	75.3	135	8	Ado47735	Ado47735 Humanised
42	483.5	75.3	139	2	Aaw65774	Aaw65774 Anti-huma
43	483.5	75.3	139	2	Aaw65773	Aaw65773 Anti-huma
44	483.5	75.3	139	2	Aaw62205	Aaw62205 Humanised
45	483.5	75.3	139	2	Aaw62206	Aaw62206 Humanised

ALIGNMENTS

RESULT 1
AAW84097

ID   AAW84097 standard; protein; 117 AA.
XX
AC   AAW84097;
XX
DT   15-MAR-1999 (first entry)
XX
DE   Humanised anti-alpha-v beta-3 MAb D12H2HC 1-0 VH.
XX
KW   Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW   mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
KW   metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;
KW   diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
KW   Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
KW   immunotherapy; D12H2HC-10.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT
FT   Region   31..35
FT   /label= CDR1
FT   Region   50..66
FT   /label= CDR2
FT   Region   99..106
FT   /label= CDR3
XX
PN   WO9840488-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998; 98WO-US004987.
XX
PR   12-MAR-1997; 97US-0039609P.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI   Jonak ZL, Johanson KO, Taylor AH;
XX
DR   WPI; 1999-034590/03.
DR   N-PSDB; AAV71799.
XX
PT   New anti alpha-v beta 3 vitronectin receptor antibodies - used for
PT   immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory
PT   disorders, atherosclerosis, restenosis, cancers or osteoporosis.
XX
PS   Claim 1; Page 58; 97pp; English.

XX
CC   This is the amino acid sequence of the heavy chain variable region (VH)
CC   of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody
CC   D12H2HC 1-0. It is based on the VH sequence (see AAW84095) of human Kabat
CC   subgroup I VH, with complementarity determining regions (CDRs) from the
CC   murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC   D12 (see AAW84093). 7 Murine framework residues (24, 48, 67, 68, 70, 72
CC   and 74) are retained. The humanised heavy chain can be expressed in host
CC   cells using nucleic acid molecules (see AAV71799) of the invention.
CC   Humanised D12 VL is also provided (see AAW84098)). The humanised
CC   antibodies can be used for passive immunotherapy of disorders mediated by
CC   the alpha-v beta-3 receptor, e.g. cardiovascular or angiogenic-related
CC   disorders, such as angiogenesis associated with diabetic retinopathy,
CC   atherosclerosis and restenosis, chronic inflammatory disorders, macular
CC   degeneration, rheumatoid arthritis and cancer, e.g. solid tumour
CC   metastasis, and diseases where bone resorption is associated with
CC   pathology such as osteoporosis, hyperparathyroidism, Paget's disease,
CC   hypercalcemia of malignancy, osteolytic lesions produced by bone
CC   metastasis, bone loss due to immobilisation or sex hormone deficiency.
CC   They can also be used for targeted drug therapy, and for detection and
CC   diagnosis
XX
SQ   Sequence 117 AA;

Query Match   82.6%; Score 530; DB 2; Length 117;
Best Local Similarity   85.1%; Pred. No. 7.7e-39;
Matches 103; Conservative 7; Mismatches 5; Indels 6; Gaps 2;

Qy   1 EVQLVQSGAEVKKPGASVKVSCKVSGYAFTNYNMYWVRQAPCKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||| :||||:||||||||||||| |||||||||||| ||| |
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYNMYWVRQAPGQGLEWIGYIDPYNGDTFY 60

Qy   61 SQFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARR--GNFPYYFDYWGQGTLVTVS 118
              :|||||||||||||||||||||||||||||||||||| |||:||||||||||||||
Db   61 NQFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARQNYGSFA----YWGQGTLVTVS 116

Db   117 S 117
Qy   119 | 119
              119 S 117

RESULT 2
AAW71880
ID   AAW71880 standard; protein; 588 AA.
XX
AC   AAW71880;
XX
DT   18-JAN-1999 (first entry)
XX
DE   Anti-human Fas humanised antibody CH11 heavy chain HmuH.
XX
KW   Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
KW   autoimmune disease; rheumatoid arthritis; therapy; human;
KW   antibody engineering.
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..19
FT   /label= Sig_peptide
FT   Protein   20..588
FT   /label= Mat_protein
FT   Region   50..54
FT   /label= CDR1
FT   /note= "complementarity determining region 1 from CH11
FT   heavy chain"
FT   Region   69..84
FT   /label= CDR2
FT   /note= "complementarity determining region 2 from CH11
FT   heavy chain"
FT   Region   118..124
FT   /label= CDR3
FT   /note= "complementarity determining region 3 from CH11
FT   heavy chain"
XX
PN   EP866131-A2.
XX
PD   23-SEP-1998.
XX
PF   20-MAR-1998; 98EP-00302113.
XX
PR   21-MAR-1997; 97JP-00067938.
XX
PA   (SANY) SANKYO CO LTD.
XX
PI   Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;
XX
DR   WPI; 1998-482965/42.
DR   N-PSDB; AAV61363.
XX
PT   Production of anti-Fas protein humanised antibodies - for use in inducing
PT   apoptosis on Fas expressing cells in the treatment of auto:immune
PT   diseases, especially rheumatoid arthritis.
XX
PS   Claim 21; Page 105-107; 187pp; English.
XX
CC   This is the amino acid sequence of a humanised anti-Fas antibody CH11
CC   heavy chain), designated HmuH. HmuH is based on the heavy chain (see
CC   AAW71888) of murine anti-human Fas monoclonal antibody CH11. The
CC   humanised sequence was designed following selection of donor residues
CC   from CH11 to be grafted onto acceptor molecule 21.28'CL, 2 Heavy chain
CC   sequences (see AAW71880-81) have been designed, and each can be used in
CC   combination with any of 4 light chain sequences (see AAW71876-79) to
CC   provide novel, claimed humanised anti-human CH11 IgM antibodies that lack a J chain.
CC   These humanised anti-human Fas antibodies are capable of inducing
CC   apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in
CC   the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA
CC   sequences encoding the humanised antibodies are claimed, as are vectors
CC   and host cells such as Escherichia coli pHmuH5-1 including the HmuH nucleotide sequence (see AAV61363),
CC   such as pHmuH5-1 (FERM BP-5863)
XX
SQ   Sequence 588 AA;

Query Match   78.6%; Score 504.5; DB 2; Length 588;
Best Local Similarity   81.7%; Pred. No. 6.6e-36;
Matches   98; Conservative 6; Mismatches 11; Indels 5; Gaps 2;

Qy   1 EVQLVQSGAEVKKPGASVKVSCKVSGYAFTNYNMYWVRQAPCKGLEWIGYIDPYYGDPGY 60
              |||||||||||||||||||| ||:||||:||||||||||||| |||||||| | || | |
Db   20 EVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNMHWVRQAPGQGLEWMGYIYPYNGGTGY 79

Qy   61 SQFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYY-FDYWGQGTLVTVSS 119
              :||||||||||||| :|||||||||||||||||||||| ||| || ||||||||||||||
Db   80 NQFKGKATLTVDKSNASTAYMELSSLRSEDTAVYYCAR-----SYYAMDYWGQGTLVTVSS 135

RESULT 3
AAB12917
ID   AAB12917 standard; protein; 588 AA.
XX
AC   AAB12917;
XX
DT   16-NOV-2000 (first entry)
XX
DE   Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.
XX
KW   Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW   immunosuppression; autoimmune disease; treatment; rheumatism;
KW   anti-Fas antibody.
OS   Synthetic.
XX
PN   JP2000154149-A.
XX
PD   06-JUN-2000.

XX
PF   17-SEP-1999; 99JP-00263984.
XX
PR   18-SEP-1998; 98JP-00264598.
XX
PA   (SANY) SANKYO CO LTD.
XX
DR   WPI; 2000-454476/40.
DR   N-PSDB; AAA78271.
XX
PT   Anti-human Fas humanizing antibody-containing antirheumatic agents.
XX
PS   Claim 1; Page 75-77; 109pp; Japanese.
XX
CC   The present invention relates to antirheumatic agents which comprise as
CC   active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC   does not include a J segment, has apoptosis inducing activity, and
CC   consists of a light and heavy chain polypeptide produced synthetically.
CC   The agents of the invention exhibit antirheumatic and immunosuppresive
CC   activity and can be used to treat autoimmune diseases, especially
CC   rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC   binding properties. Included in the invention are nucleotide sequences of
CC   the IgM light and heavy chains (see AAB12913-B12918 and AAB12919), and
CC   corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC   nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC   AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC   included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC   Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC   chains used in the invention are represented by sequences AAA78213-
CC   A78266. Primers used for sequencing the human Ig DNA used in the
CC   invention are represented by sequences AAA78277-A78318 and AAA78335-
CC   A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC   represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
CC   sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
CC   the production of the agent of the invention
XX
SQ   Sequence 588 AA;

Query Match   78.6%; Score 504.5; DB 3; Length 588;
Best Local Similarity   81.7%; Pred. No. 6.6e-36;
Matches   98; Conservative   6; Mismatches   11; Indels   5; Gaps   2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 EVQLVQSGAEVKKPGASVKYSCKASGYTFTDYNMHWVRQAPGQGLEWMGYIYPYNGGTGY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYY-PDYWGQGTLVTVSS 119
              ||:|||||||||||||||||||||||||||||||||||| ||| ||||||||||||
Db   80 NQKFKGKATLTVDNSASTAYMELSSLRSEDTAVYYCAR----SYYAMDYWGQGTLVTVSS 135

RESULT 4
AD L11892
ID   AD L11892 standard; peptide; 117 AA.
XX
AC   AD L11892;
XX
DT   06-MAY-2004 (first entry)
XX
DE   CDR transplant antibody heavy chain variable region #3.
XX
KW   receptor Flt-1; Cytostatic; lung cancer; CDR.
KW   cancer metastasis; human vascular endothelial growth factor; VEGFr;
XX
OS   Homo sapiens.
XX
PN   JP2003261460-A.
XX
PD   16-SEP-2003.
XX
PF   08-MAR-2002; 2002JP-0063835.
PR   08-MAR-2002; 2002JP-0063835.

--- column 2 ---

XX
PA   (KYOW) KYOWA HAKKO KOGYO KK.
PA   (SHIB) SHIBUYA T.
XX
DR   WPI; 2004-056096/06.
XX
PT   Preventive or therapeutic agent of lung selective cancer metastasis
PT   containing the substance which inhibits the information transmission
PT   which intervenes human VEGF receptor Flt-1 as an active ingredient.
XX
PS   Claim 18; SEQ ID NO 19; 36pp; Japanese.
XX
CC   The present invention relates to a preventive or therapeutic agent of
CC   lung selective cancer metastasis containing the substance which inhibits
CC   the information transmission which intervenes human vascular endothelial
CC   growth factor (VEGF) receptor Flt-1 as an active ingredient. The
CC   invention is useful for inhibiting spread of lung cancer, and effectively
CC   controls the spread of lung cancer. The present sequence represents a CDR
CC   transplant antibody heavy chain variable region.
XX
SQ   Sequence 117 AA;

Query Match   78.5%; Score 504; DB 8; Length 117;
Best Local Similarity   80.7%; Pred. No. 1.5e-36;
Matches   96; Conservative   9; Mismatches   12; Indels   2; Gaps   1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              |||||||||||||||||||||||::|||||||||||||||||||||||:|||||||
Db   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPGNGTSY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYYPDYWGQGTLVTVSS 119
              |||||||:||||||||||||||||||||||||||||| | :||||||||||||||||
Db   61 NQKFKGRVTITVDKSTSTAYMELSSLRSEDTAVYYCARDGD--YYFDYWGQGTLVTVSS 117

RESULT 5
AAY77596
ID   AAY77596 standard; peptide; 136 AA.
XX
AC   AAY77596;
XX
DT   08-MAY-2000 (first entry)
XX
DE   Anti-human VEGF receptor Flt-1 antibody related peptide sequence #91.
XX
KW   Flt-1; neovascularisation; cell proliferation; metastasis; tumour;
KW   Antibody; human; vascular endothelial growth factor; VEGF receptor;
KW   rheumatoid arthritis; retinopathy; psoriasis.
XX
OS   Mus musculus.
XX
PN   WO960025-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999; 99WO-JP002661.
PR   20-MAY-1998; 98JP-00139000.
XX
PA   (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K, Ito M, Kawada Y, Nakamura K;
XX
DR   WPI; 2000-072431/06.
DR   N-PSDB; AAZ87738.
XX
PT   Gene recombinant antibodies, useful for diagnosis and as remedies for
PT   diseases due to abnormal neovascularization e.g. proliferation or
PT   metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy and
PT   psoriasis.
XX
PS   Claim 28; Page 199-200; 210pp; Japanese.

```
CC   The invention relates to a gene recombinant antibody that has specific
CC   reaction with human vascular endothelial growth factor (VEGF) receptor
CC   Flt-1. The antibodies are useful for diagnosis and as remedies for
CC   diseases due to abnormal neovascularisation such as proliferation or
CC   metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
CC   retinopathy, premature retinopathy and psoriasis
XX
SQ   Sequence 136 AA;

Query Match             78.5%;  Score 504;  DB 3;  Length 136;
Best Local Similarity   80.7%;  Pred. No. 1.7e-36;
Matches    96;  Conservative    9;  Mismatches  12;  Indels    2;  Gaps    1;

Qy    1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY   60
         :|||||:||||||||||||||||::|:|||||||||:::|||||||||||:||:||||||
Db   20  QVQLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPGNGFTSY   79

Qy   61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS  119
         :|||||:|||:|||:||||||||||||||||||||||:|||:   :||||||||||||
Db   80  NQKFKGRVTITVDKSTSTAYMELSSLRSEDTAVYYCARDGD--YYFDYWGQGTLVTVSS  136
```

```
RESULT 6
AAB78865
ID   AAB78865 standard; protein; 136 AA.
XX
AC   AAB78865;
XX
DT   20-APR-2001  (first entry)
XX
DE   Anti-human Flt-1 antibody VH CDR protein sequence SEQ ID 87.
XX
KW   Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
KW   vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
KW   delayed hypersensitivity; malignant tumour; arteriosclerosis.
XX
OS   Synthetic.
XX
PN   WO20007927S-A1.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-JP003957.
XX
PR   17-JUN-1999;  99JP-0171709.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K, Shibuya M;
XX
PT   WPI; 2001-080847/09.
XX
DR   Substances binding to human vascular endothelial growth factor receptor
DR   Flt-1, used for diagnosis and treatment of inflammatory diseases,
DR   arteriosclerosis, cancer and delayed hypersensitivity.
XX
PS   Example 3; Page 155; 164pp; Japanese.
XX
CC   This invention relates to a reagent for detecting differentiation of
CC   monocytes and macrophages from haematopoietic stem cells, containing a
CC   substance which binds to human vascular endothelial growth factor (VEGF)
CC   receptor Flt-1. The invention also includes a method for diagnosing a
CC   disease in which the differentiation of monocytes and macrophages is
CC   implicated, using the reagent, and an agent for the treatment of diseases
CC   diagnosed using the method, containing a substance which binds to Flt-1
CC   or a substance which inhibits the signal transduction of Flt-1. Diseases
CC   which may be diagnosed or treated include inflammation, delayed
CC   hypersensitivity, malignant tumours and arteriosclerosis. AAF70190 -
CC   AAF70244, AAF70251 and AAF70258 represent DNA sequences encoding anti-
CC   human Flt-1 monoclonal antibody fragments, and oligonucleotides used in
CC   the construction of the antibody. The monoclonal antibody is used in the
CC   reagent of the invention. PCR primers AAF70245 - AAF70870 (excluding
CC   AAF70251) are used in the isolation of the antibody DNA sequences.
```

```
CC   Protein sequences AAB78848 - AAB78870 represent fragments of the anti-
CC   human Flt-1 antibody
XX
SQ   Sequence 136 AA;

Query Match             78.5%;  Score 504;  DB 4;  Length 136;
Best Local Similarity   80.7%;  Pred. No. 1.7e-36;
Matches    96;  Conservative    9;  Mismatches  12;  Indels    2;  Gaps    1;

Qy    1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY   60
         :|||||:||||||||||||||||::|:|||||||||:::|||||||||||:||:||||||
Db   20  QVQLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPGNGFTSY   79

Qy   61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS  119
         :|||||:|||:|||:||||||||||||||||||||||:|||:   :||||||||||||
Db   80  NQKFKGRVTITVDKSTSTAYMELSSLRSEDTAVYYCARDGD--YYFDYWGQGTLVTVSS  136
```

```
RESULT 7
AAW84099
ID   AAW84099 standard; protein; 110 AA.
XX
AC   AAW84099;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Vitronectin alpha-v beta-3 MAb VH.
XX
KW   Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW   mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
KW   metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;
KW   diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
KW   Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
KW   immunotherapy.
XX
OS   Mus sp.
XX
PN   WO9840488-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998;  98WO-US004987.
XX
PR   12-MAR-1997;  97US-0039609P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Jonak ZL, Johanson KO, Taylor AH;
XX
PT   WPI; 1999-034590/03.
PT   N-PSDB; AAV71801.
XX
DR   New anti alpha-v beta_3 vitronectin receptor antibodies - used for
DR   immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory
DR   disorders, atherosclerosis, restenosis, cancers or osteoporosis.
XX
PS   Example 13; Page 63; 97pp; English.
XX
CC   This is the amino acid sequence of the region of the murine monoclonal
CC   antibody (MAb) D12 heavy chain variable region (VH) that is altered in
CC   humanised D12 VH (see also AAW84097). A synthetic gene (see AAV81901)
CC   encoding the protein was prepared from synthetic oligonucleotides
CC   used to prepare an expression vector for humanised D12 VH. D12 is an anti
CC   -human alpha-v beta-3 vitronectin receptor MAb. Humanised D12 MAbs can be
CC   used for passive immunotherapy of disorders mediated by the alpha-v beta-
CC   3 vitronectin receptor, e.g. restenosis and angiogenic associated
CC   diseases
XX
SQ   Sequence 110 AA;

Query Match             78.3%;  Score 503;  DB 2;  Length 110;
Best Local Similarity   85.1%;  Pred. No. 1.7e-36;
Matches    97;  Conservative    6;  Mismatches   5;  Indels    6;  Gaps    2;
```

Qy   3 QLVQSGAEVKKPGASVKISCKVSGYTAFTNYNMYWYRQAPGKGLEWIGYIDPYYGPGYSQ 62
        ||||||||||||||| ||||| ||||| ||||||:||||| |||||||||||| | :|
Db   1 QLVQSGAEVKKPGASVKKPGASVKVSCKASGYAFTSYNMYWVRQAPGQGLEWIGYIDPYNGDTFYNQ 60

Qy   63 KFPGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARR--GNFPYYFDYWGQGTL 114
        ||||||||||||||||||||||||||||||||||| :|:
Db   61 KFPGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARQNYGSFA----YWGQGTL 110

```
RESULT 8
XX
ID   AAR29017
XX
AC   AAR29017;
XX
DT   25-MAR-2003  (revised)
DT   30-MAR-1993  (first entry)
XX
DE   AAR29017 standard; protein; 135 AA.
XX
DE   pUC-RVh-1220d.
XX
KW   Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW   complementarity determining region; monoclonal; hybridoma; PCR; plasmid;
KW   polymerase chain reaction; amplify.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FH
FT   Peptide         1..19
FT                   /note= "Leader peptide"
FT   Region          20..49
FT                   /label= FR1
FT   Region          50..54
FT                   /label= CDR1
FT   Region          55..68
FT                   /label= FR2
FT   Region          69..85
FT                   /label= CDR2
FT   Region          86..117
FT                   /label= FR3
FT   Region          118..124
FT                   /label= CDR3
FT   Region          125..135
FT                   /label= FR4
XX
PN   WO9219759-A1.
XX
PD   12-NOV-1992.
XX
PF   24-APR-1992;   92WO-JP000544.
XX
PR   25-APR-1991;   91JP-00095476.
PR   19-FEB-1992;   92JP-00032084.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;
XX
DR   WPI; 1992-398882/48.
DR   N-PSDB; AAQ31391.
XX
PT   Reconstituted human antibody to human interleukin-6 receptor - has low
PT   antigenicity and contains mouse V-region complementarily determining
PT   regions.
XX
PS   Disclosure; Page 159-60; 207pp; Japanese.
XX
CC   The sequences given in AAR29016-17 are portions of monoclonal antibodies
CC   which were encoded by plasmids contained within the mouse hybridoma,
CC   AUK12-20. The DNA encoding the complementarity determining regions
CC   (CDR's) was isolated by polymerase chain reaction. These antibodies
CC   recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were
CC   transformed with plasmids containing fragments of the antibody gene which
CC   caused the production of the antibody from the hybridoma cell line.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 135 AA;
```

Query Match   77.5%;   Score 497.5;   DB 2;   Length 135;
Best Local Similarity   79.0%;   Pred. No. 6.2e-36;
Matches   94;   Conservative 11;   Mismatches 11;   Indels 3;   Gaps 1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYTAFTNYNMYWYRQAPGKGLEWIGYIDPYYGPGY 60
        :||||||||||||||| ||||| ||||| ||||||:||||| |||||||||||| |
Db   20 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWIGYIDPENGGTSY 79

Qy   61 SQKFPGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
        ||||||||||||||||||||||||||||| |:|||
Db   80 NQKFPGKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGN---RFAYWGQGTLVTVSS 135

```
RESULT 9
XX
ID   AAW22418
XX
AC   AAW22418;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Reshaped human AUK12-20 VH.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma;
KW   atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis;
KW   inflammatory bowel disease; rheumatoid arthritis; transplant rejection;
KW   graft versus host disease; nephritis; atopic dermatitis; psoriasis;
KW   myocardial ischaemia; acute leukocyte mediated lung injury; therapy;
KW   AUK12-20.
XX
OS   Homo; sapiens.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FH
FT   Region          1..30
FT                   /label= FR1
FT   Region          31..35
FT                   /label= CDR1
FT   Region          36..49
FT                   /label= FR2
FT   Region          50..66
FT                   /label= CDR2
FT   Region          67..98
FT                   /label= FR3
FT   Region          99..105
FT                   /label= CDR3
FT   Region          106..116
FT                   /label= FR4
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US018807.
XX
PR   21-NOV-1995;   95US-00561521.
XX
PA   (ATHB-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM, Leger OJ, Saldanha J, Jones ST, Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of asthma,
PT   atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Page 44; 107pp; English.
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```
XX
CC   This polypeptide comprises version 'b', of a reshaped human antibody
CC   AUK12-20 VH region. A DNA fragment encoding the polypeptide was subcloned
CC   into vector pUC19 for use as a template for PCR amplification and
CC   production of version 'a', of a reshaped human 21.6 VH region (see
CC   AAW22413) that can be used in the construction of novel humanised anti-
CC   alpha-4 integrin antibodies. Claimed humanised antibodies are useful in
CC   the treatment of asthma, atherosclerosis, AIDS, dementia, diabetes,
CC   inflammatory bowel disease, rheumatoid arthritis, transplant rejection,
CC   graft versus host disease, tumour metastasis, nephritis, atopic
CC   dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated
CC   lung injury.
XX
SQ   Sequence 116 AA;

Query Match             77.3%;  Score 496.5;  DB 2;  Length 116;
Best Local Similarity   78.2%;  Pred. No. 6.6e-36;
Matches   93;  Conservative  12;  Mismatches  11;  Indels   3;  Gaps   1;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              ::|||||||||||||||||:|:||:|||||:|| |:|::|:|||||||||||||| ||||
Db          1 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWVGYIDPFNGGTSY 60

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              |||||||| |:||:||:|||||||||||||||||||||   | ||||||||||||||||
Db         61 NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGN---RFAYWGQGTLVTVSS 116
```

```
RESULT 10
AAR29016
ID   AAR29016 standard; protein; 135 AA.
XX
AC   AAR29016;
XX
DT   25-MAR-2003  (revised)
DT   30-MAR-1993  (first entry)
XX
DE   pUC-RVh-1220b.
XX
KW   Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW   complementarity determining region; monoclonal; hybridoma; PCR; plasmid;
KW   polymerase chain reaction; amplify.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "Leader peptide"
FT   Region          20..49
FT                   /label= FR1
FT   Region          50..54
FT                   /label= CDR1
FT   Region          55..68
FT                   /label= FR2
FT   Region          69..85
FT                   /label= CDR2
FT   Region          86..117
FT                   /label= FR3
FT   Region          118..124
FT                   /label= CDR3
FT   Region          125..135
FT                   /label= FR4
XX
PN   WO9219759-A1.
PD   12-NOV-1992.
XX
PF   24-APR-1992; 92WO-JP000544.
XX
PR   25-APR-1991; 91JP-0095476.
PR   19-FEB-1992; 92JP-0003284.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;
XX
DR   WPI; 1992-398882/48.
DR   N-PSDB; AAQ31391.
XX
PT   Reconstituted human antibody to human interleukin-6 receptor - has low
PT   antigenicity and contains mouse V-region complementarily determining
PT   regions.
XX
CC   Disclosure; Page 157-8; 207pp; Japanese.
XX
CC   The sequences given in AAR29016-17 are portions of monoclonal antibodies
CC   which were encoded by plasmids contained within the mouse hybridoma,
CC   AUK12-20. The DNA encoding the complementarity determining regions
CC   (CDR's) was isolated by polymerase chain reaction. These antibodies
CC   recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were
CC   transformed with plasmids containing fragments of the antibody which
CC   caused the production of the antibody from the hybridoma cell line.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 135 AA;

Query Match             77.3%;  Score 496.5;  DB 2;  Length 135;
Best Local Similarity   78.2%;  Pred. No. 7.6e-36;
Matches   93;  Conservative  12;  Mismatches  11;  Indels   3;  Gaps   1;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              ::|||||||||||||||||:|:||:|||||:|| |:|::|:|||||||||||||| ||||
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWVGYIDPFNGGTSY 79

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              |||||||| |:||:||:|||||||||||||||||||||   | ||||||||||||||||
Db         80 NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGN---RFAYWGQGTLVTVSS 135
```

```
RESULT 11
AAW73187
ID   AAW73187 standard; protein; 144 AA.
XX
AC   AAW73187;
XX
DT   22-JAN-1999  (first entry)
XX
DE   Fragment of ganglioside GM2 targeting antibody.
XX
KW   Ganglioside GM2; antibody; complementarity determining region; cancer;
KW   anti-tumour agent.
OS   Homo sapiens.
XX
PN   JP10257893-A.
XX
PD   29-SEP-1998.
XX
PF   19-MAR-1997;  97JP-00066981.
XX
PR   19-MAR-1997;  97JP-00066981.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
DR   WPI; 1998-575904/49.
DR   N-PSDB; AAV08097.
XX
PT   A human type complementarity determining region transplanted antibody
PT   against ganglioside GM2 - useful as an anti-tumour agent and as a
PT   diagnostic for related cancers.
XX
PS   Example 4; Page 46-47; 66pp; Japanese.
XX
CC   This sequence is a fragment of an antibody of the invention. The antibody
CC   of the invention is a human complementarity determining region
CC   transplanted antibody that reacts specifically with ganglioside GM2. DNA
```

```
CC   encoding the antibody, and vectors and transformants containing it, can
CC   be used for the recombinant production of the antibody. The antibody
CC   itself can be used as an anti-tumour agent or as a diagnostic tool for
CC   related cancers. The antibody has antitumour activity against ganglioside
CC   GM2 positive cells
XX
SQ   Sequence 144 AA;

Query Match             76.7%;  Score 492.5;  DB 2;  Length 144;
Best Local Similarity   80.0%;
Matches   96;  Conservative    7;  Mismatches  16;  Indels    1;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWYWRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||:|||||||||| || |||||||||:||:|:||||||||||
Db         20 EVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNMDWVRQAPGQGLEWMGYIYPNNGGTGY 79

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGN-FPYYFDYWGQGTLVTVSS 119
              :||||| |:|||||||||||||||||||||||||||||||| |:|| ||||||||||||
Db         80 NQKFKSKATLTVDTSTSTAYMELHSLRSEDRAVYYCATYGHYYGYMFAYWGQGTLVTVSS 139
```

```
RESULT 12
ID   ADL11893
XX
AC   ADL11893;
XX
DT   06-MAY-2004  (first entry)
XX
DE   CDR transplant antibody heavy chain variable region #4.
XX
KW   cancer metastasis; human vascular endothelial growth factor; VEGFr;
KW   receptor Flt-1; Cytostatic; lung cancer; CDR.
XX
OS   Homo sapiens.
XX
PN   JP2003261460-A.
XX
PD   16-SEP-2003.
XX
PF   08-MAR-2002; 2002JP-00063835.
XX
PR   08-MAR-2002; 2002JP-00063835.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SHIB/) SHIBUYA T.
XX
DR   WPI; 2004-056096/06.
XX
PT   Preventive or therapeutic agent of lung selective cancer metastasis
PT   containing the substance which inhibits the information transmission
PT   which intervenes human VEGF receptor Flt-1 as an active ingredient.
XX
PS   Claim 18; SEQ ID NO 20; 36pp; Japanese.
XX
CC   The present invention relates to a preventive or therapeutic agent of
CC   lung selective cancer metastasis containing the substance which inhibits
CC   the information transmission which intervenes human vascular endothelial
CC   growth factor (VEGF) receptor Flt-1 as an active ingredient. The
CC   invention is useful for inhibiting spread of lung cancer, and effectively
CC   controls the spread of lung cancer. The present sequence represents a CDR
CC   transplant antibody heavy chain variable region.
XX
SQ   Sequence 117 AA;

Query Match             76.6%;  Score 492;  DB 8;  Length 117;
Best Local Similarity   78.2%;  Pred. No. 1.6e-35;
Matches   93;  Conservative   11;  Mismatches  13;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWYWRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||:|||||||||| || |||||||||:||:|:||||||||||
Db          1 QVQLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPNGFTSY 60
```

```
RESULT 13
ID   AAY77600
XX
AC   AAY77600;
XX
DT   08-MAY-2000  (first entry)
XX
DE   Anti-human VEGF receptor Flt-1 antibody related peptide sequence #95.
XX
KW   Antibody; human; vascular endothelial growth factor; VEGF receptor;
KW   Flt-1; neovascularisation; cell proliferation; metastasis; tumour;
KW   rheumatoid arthritis; retinopathy; psoriasis.
XX
OS   Mus musculus.
XX
PN   WO9960025-A1.
XX
PD   25-NOV-1999.
XX
PF   20-MAY-1999;  99WO-JP002661.
XX
PR   20-MAY-1998;  98JP-00139000.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K, Ito M, Kawada Y, Nakamura K;
XX
DR   WPI; 2000-072431/06.
DR   N-PSDB; AA287778.
XX
PT   Gene recombinant antibodies, useful for diagnosis and as remedies for
PT   diseases due to abnormal neovascularization e.g. proliferation or
PT   metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy and
PT   psoriasis.
XX
PS   Claim 28; Page 203; 210pp; Japanese.
XX
CC   The invention relates to a gene recombinant antibody that has specific
CC   reaction with human vascular endothelial growth factor (VEGF) receptor
CC   Flt-1. The antibodies are useful for diagnosis and as remedies for
CC   diseases due to abnormal neovascularisation such as proliferation or
CC   metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
CC   retinopathy, premature retinopathy and psoriasis
XX
SQ   Sequence 136 AA;

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              :||||||||||||||||||||||||||||||||||||||:  ||||||||||||||||
Db         61 NQKFKGRVTITVDKSTSTAYMQLRSLRSEDTAVYFCARDGD--YYFDYWGQGTLVTVSS 117
```

```
Query Match             76.6%;  Score 492;  DB 3;  Length 136;
Best Local Similarity   78.2%;  Pred. No. 1.9e-35;
Matches   93;  Conservative   11;  Mismatches  13;  Indels    2;  Gaps    1;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWYWRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||:|||||||||| || |||||||||:||:|:||||||||||
Db         20 QVQLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPNGFTSY 79

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              :||||||||||||||||||||||||||||||||||||||:  ||||||||||||||||
Db         80 NQKFKGRVTITVDKSTSTAYMQLRSLRSEDTAVYFCARDGD--YYFDYWGQGTLVTVSS 136
```

```
RESULT 14
ID   AAB78869
XX
AC   AAB78869;
XX
DT   20-APR-2001  (first entry)
```

```
DE   Anti-human Flt-1 antibody VH CDR protein sequence SEQ ID 91.
XX
KW   Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
KW   vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
KW   delayed hypersensitivity; malignant tumour; arteriosclerosis.
XX
OS   Synthetic.
XX
PN   WO200079275-A1.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-1999; 2000WO-JP003957.
XX
PR   17-JUN-1999; 99JP-0017170 9.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K, Shibuya M;
XX
DR   WPI; 2001-080847/09.
DR   N-PSDB; AAF70251.
XX
PT   Substances binding to human vascular endothelial growth factor receptor
PT   Flt-1, used for diagnosis and treatment of inflammatory diseases,
PT   arteriosclerosis, cancer and delayed hypersensitivity.
XX
PS   Example 3; Page 157-158; 164pp; Japanese.
XX
CC   This invention relates to a reagent for detecting differentiation of
CC   monocytes and macrophages from haematopoietic stem cells, containing a
CC   substance which binds to human vascular endothelial growth factor (VEGF)
CC   receptor Flt-1. The invention also includes a method for diagnosing a
CC   disease in which the differentiation of monocytes and macrophages is
CC   implicated, using the reagent, and an agent for the treatment of diseases
CC   diagnosed using the method, containing a substance which binds to Flt-1
CC   or a substance which inhibits the signal transduction of Flt-1. Diseases
CC   which may be diagnosed or treated include inflammation, delayed
CC   hypersensitivity, malignant tumours and arteriosclerosis. AAF70190 -
CC   AAF70244, AAF70251 and AAF70258 represent DNA sequences encoding anti-
CC   human Flt-1 monoclonal antibody fragments, and oligonucleotides used in
CC   the construction of the antibody. The monoclonal antibody is used in
CC   the reagent of the invention. PCR primers AAF70245 - AAF70870 (excluding
CC   AAF70251) are used in the isolation of the antibody DNA sequences.
CC   Protein sequences AAB78848 - AAB78870 represent fragments of the anti-
CC   human Flt-1 antibody
XX
SQ   Sequence 136 AA;

Query Match             76.6%;  Score 492;  DB 4;  Length 136;
Best Local Similarity   78.2%;  Pred. No. 1.9e-35;
Matches   93;  Conservative   11;  Mismatches   13;  Indels    2;  Gaps    1;

Qy    1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMHWVRQAPGKGLEWIGYIDPYYGDGY  60
         |||||||||||||||||||||||:||| ||||||||||||||||||||||:||||||
Db   20  QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYNMHWVRQAPGQGLEWMGAIFPGNGFTSY  79

Qy   61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
         :|||||:|:||||||||||||||||||||||||||||||||:||||||||||||||||
Db   80  NQKFKGRVTITVDKSTSTAYMQLRSLRSEDTAVFFCARDGD--YYFDYWGQGTLVTVSS 136
```

```
RESULT 15
ID   AAB07965 standard; protein; 135 AA.
XX
AC   AAB07965;
XX
DT   14-NOV-2000  (first entry)
XX
DE   A heavy chain variable region of humanised 3S1 antibody.
XX
KW   Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW   autoimmune disease; infectious disease; inflammatory disorder;
KW   systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW   arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW   multiple sclerosis; transplant rejection; proliferative disease;
KW   leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW   aplastic anaemia; myeloid dysplasia syndrome.
XX
OS   Synthetic.
OS   Mus sp.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Protein         20..135
FT                   /note= "mature protein"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          118..124
FT                   /note= "complementarity determining region 3"
XX
PN   WO200047625-A2.
XX
PD   17-AUG-2000.
XX
PF   09-FEB-2000; 2000WO-US003303.
XX
PR   12-FEB-1999; 99US-00249011.
PR   24-JUN-1999; 99US-00339596.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Co MS, Vasquez M, Carreno B, Celniker AC, Collins M,
PI   Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR   WPI; 2000-524532/47.
DR   N-PSDB; AAA59694.
XX
PT   Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT   from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT   modulates immune responses and can therefore treat e.g. autoimmune
PT   diseases, infectious diseases.
XX
PS   Example 3; Fig 2A; 162pp; English.
XX
CC   The present sequence represents the heavy chain variable region of the
CC   humanised murine antibody 3D1. The antibody has a binding specificity to
CC   B7 molecules. The antibody is used to construct humanized
CC   immunoglobulins, which comprise an antigen binding region of non-human
CC   origin and a portion of a human immunoglobulin. The humanized
CC   immunoglobulins are useful for treating autoimmune diseases, infectious
CC   diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC   mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC   inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC   also useful for treating a transplant recipient, and treating
CC   rejection in a transplant recipient, and treating proliferative disease
CC   (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC   thalassemia and aplastic anaemia), inborn errors of metabolism,
CC   congenital immunodeficiency diseases, and myeloid dysplasia syndrome
XX
SQ   Sequence 135 AA;

Query Match             76.4%;  Score 490.5;  DB 3;  Length 135;
Best Local Similarity   78.2%;  Pred. No. 2.6e-35;
Matches   93;  Conservative   11;  Mismatches   12;  Indels    3;  Gaps    1;

Qy    1  EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMHWVRQAPGKGLEWIGYIDPYYGDGY  60
         |||||||||||||||||||||||:||| ||||||||||||||||||:||| ||:||||
Db   20  QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYAIQWVRQAPGQGLEWMGVINIYYDNTNY  79

Qy   61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
```

Db   80 NQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA---WYMDYWGQGTLVTVSS 135
              :|||||||:|:|||||||||||||||||||||||||||||||||| :| |||||||||||||||

Search completed: December 29, 2004, 17:57:34
Job time : 83.7906 secs

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OM protein - protein search, using sw model

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                        GenCore version 5.1.6
                        Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:                 December 29, 2004, 18:05:34 ; Search time 68.8024 seconds
                                               (without alignments)
                                               622.182 Million cell updates/sec

Title:          US-10-774-076-12
Perfect score:  642
Sequence:       1 EVQLVQSGAEVKKPGASVKI.........GNFPYYFDYWGQGTLVTVSS 119
Scoring table:  Gapop 10.0 , Gapext 0.5
Searched:       1599051 seqs, 359727711 residues
Total number of hits satisfying chosen parameters:   1599051

Database :      BLOSUM62
                Minimum Match 0%
                Listing first 45 summaries

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

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    2: /cgn2_6/ptodata/2/pubpaa/US06_PCT_NEW_PUB.pep:*
    3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
    4: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep:*
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    7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
    8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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   10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
   11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
   12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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   15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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   18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
   19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
   20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

    .Published_Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	642	100.0	119	17	US-10-774-076-12	Sequence 12, Appl
2	642	100.0	138	17	US-10-774-076-17	Sequence 17, Appl
3	564	87.9	119	17	US-10-774-076-2	Sequence 2, Appli
4	564	87.9	138	17	US-10-774-076-9	Sequence 9, Appli
5	530	82.6	117	14	US-10-223-880-5	Sequence 5, Appli
6	504	78.5	136	14	US-10-160-232-91	Sequence 91, Appl
7	503	78.3	110	14	US-10-223-880-12	Sequence 12, Appl
8	492	76.6	136	14	US-10-160-232-95	Sequence 95, Appl
9	490.5	76.4	135	9	US-09-249-011A-6	Sequence 6, Appl
10	490.5	76.4	461	9	US-09-249-011A-24	Sequence 24, Appl
11	488.5	76.1	116	14	US-10-389-155-16	Sequence 16, Appl
12	488.5	76.1	116	15	US-10-389-417-16	Sequence 16, Appl
13	488.5	76.1	116	15	US-10-452-357-57	Sequence 57, Appl

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14  486.5  75.8  118  14  US-10-148-844-43       Sequence 43, Appl
15  483.5  75.3  116  14  US-10-127-890-169      Sequence 169, App
16  483.5  75.3  116  14  US-10-340-189-86       Sequence 86, Appl
17  483.5  75.3  116  14  US-10-389-155-25       Sequence 25, Appl
18  483.5  75.3  116  15  US-10-325-696-55       Sequence 55, Appl
19  483.5  75.3  116  15  US-10-389-417-25       Sequence 25, Appl
20  483.5  75.3  135  15  US-10-389-155-32       Sequence 32, Appl
21  483.5  75.3  135  15  US-10-389-417-32       Sequence 32, Appl
22  483.5  75.3  135  15  US-10-452-357-19       Sequence 19, Appl
23  483.5  75.3  135  15  US-09-760-723-7        Sequence 7, Appli
24  483.5  75.3  139  9   US-09-760-723-7        Sequence 7, Appli
25  483.5  75.3  139  9   US-09-355-925-7        Sequence 7, Appli
26  483.5  75.3  139  9   US-09-355-925-8        Sequence 8, Appli
27  483.5  75.3  139  10  US-09-269-921-125      Sequence 125, App
28  483.5  75.3  139  10  US-09-269-921-128      Sequence 128, App
29  483.5  75.3  139  10  US-09-509-098-50       Sequence 50, Appl
30  483.5  75.3  139  10  US-09-509-098-127      Sequence 127, App
31  483.5  75.3  139  14  US-10-315-125-7        Sequence 7, Appli
32  483.5  75.3  139  14  US-10-315-125-8        Sequence 8, Appli
33  483.5  75.3  139  14  US-10-218-253-125      Sequence 125, App
34  483.5  75.3  139  14  US-10-218-253-128      Sequence 128, App
35  483.5  75.3  139  14  US-10-428-085-7        Sequence 7, Appli
36  483.5  75.3  139  15  US-10-428-085-8        Sequence 8, Appli
37  483.5  75.3  139  16  US-10-474-714-6        Sequence 6, Appli
38  483    75.2  117  9   US-09-956-206A-78      Sequence 78, Appl
39  483    75.2  136  9   US-09-956-206A-63      Sequence 63, Appl
40  448    75.2  448  9   US-09-917-410-6        Sequence 6, Appli
41  482.5  75.2  139  10  US-09-269-921-111      Sequence 111, App
42  482.5  75.2  139  10  US-09-269-921-117      Sequence 117, App
43  482.5  75.2  139  10  US-09-509-098-22       Sequence 22, Appl
44  482.5  75.2  139  10  US-09-509-098-34       Sequence 34, Appl
45  482.5  75.2  139  14  US-10-218-253-111      Sequence 111, App
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ALIGNMENTS

```
RESULT 1
US-10-774-076-12
Sequence 12, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs, Inc.
;  APPLICANT: Landolfi, et al.
;  TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
;  TITLE OF INVENTION: Psoriasis
;  FILE REFERENCE: 05882.0064.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/774,076
;  CURRENT FILING DATE: 2004-02-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 12
;  LENGTH: 119
;  TYPE: PRT
;  ORGANISM: Artificial
;  FEATURE:
;  OTHER INFORMATION: Humanized antibody
US-10-774-076-12

Query Match             100.0%;  Score 642;  DB 17;  Length 119;
Best Local Similarity   100.0%;  Pred. No. 8.6e-52;
Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60

Qy         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYYFDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNPPYYFDYWGQGTLVTVSS 119

RESULT 2
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US-10-774-076-17
; Sequence 17, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 17
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody

US-10-774-076-17

Query Match   100.0%; Score 642; DB 17; Length 138;
Best Local Similarity 100.0%;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAARRGNFPYYFDYWGQGTLVTVSS 119
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAARRGNFPYYFDYWGQGTLVTVSS 138
```

RESULT 3
US-10-774-076-2
; Sequence 2, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mus sp.

US-10-774-076-2

Query Match   87.9%; Score 564; DB 17; Length 119;
Best Local Similarity 84.9%;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

```
Qy    1 EVQLVQSGAEVKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        :||:|||||||||:||||||||:|||||||||||:|||||||||||||||||||||||
Db    1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAARRGNFPYYFDYWGQGTLVTVSS 119
        ||||||||||||||:|||||:|:||:||||:|||||||||:||||||||||||||:||||
Db   61 SQKFKGKATLTVDKSSTAYMHLNSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
```

RESULT 4
US-10-774-076-9
; Sequence 9, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 9
; LENGTH: 138
; TYPE: PRT
; ORGANISM: mus sp.

US-10-774-076-9

Query Match   87.9%; Score 564; DB 17; Length 138;
Best Local Similarity 84.9%;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        :||:||||||||||||||||||:|||||||||||:|||||||||||||||||||||||||
Db   20 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAARRGNFPYYFDYWGQGTLVTVSS 119
        ||||||||||||||:|||||:|:||:||||:|||||||||:||||||||||||||:||||
Db   80 SQKFKGKATLTVDKSTSTAYMHLNSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 138
```

RESULT 5
US-10-223-880-5
; Sequence 5, Application US/10223880
; Publication No. US20030152571A1
; GENERAL INFORMATION:
; APPLICANT: JONAK, ZDENKA
; APPLICANT: JOHANSON, KYUNG O.
; APPLICANT: TAYLOR, ALEXANDER
; TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: P50629C1
; CURRENT APPLICATION NUMBER: US/10/223,880
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-223-880-5

Query Match   82.6%; Score 530; DB 14; Length 117;
Best Local Similarity 85.1%;
Matches 103; Conservative 7; Mismatches 5; Indels 6; Gaps 2;

```
Qy    1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
        :|||||||||||||||||:|||||:||||||:|||||||||||:|||||||||||||:.|
Db    1 QVQLVQSGAEVKKPGASVKVSCKASGYAFTSYNMYWVRQAPGQGLEWIGYIDPYYNGDTFY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCAARR-GNFPYYFDYWGQGTLVTVSS 119
        .|||||||||||||||||||||||||||||||||||||:    :    :||||||||||||:
Db   61 NQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARQNYGSFA----YWGQGTLVTVS 116
```

RESULT 6
US-10-160-232-91

Sequence 91, Application US/10160232
Publication No. US2003008075A1
GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/10/160,232
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 91
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-10-160-232-91

Query Match   78.5%; Score 504; DB 14; Length 136;
Best Local Similarity   80.7%; Pred. No. 5.8e-39;
Matches 96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

```
Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMHWVRQAPGKGLEWIGYIDPYYGDPGY  60
         |||||||| ||||||||||| ||| ||| |||||||||||| ||||| |  |  |  |
Db  20 QVQLVQSGGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPGNGFTSY  79

Qy  61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
        :|||:||||||||||||||||||||||||||||| :||||||||||||||||||||||
Db  80 NQKFKGRVTITVDKSTSTAYMELSSLRSEDTAVYYCARDGD--YYFDYWGQGTLVTVSS 136
```

RESULT 7
US-10-223-880-12
Sequence 12, Application US10223880
Publication No. US20030152571A1
GENERAL INFORMATION:
; APPLICANT: JONAK, ZDENKA
; APPLICANT: JOHNSON, KYUNG O.
; APPLICANT: TAYLOR, ALEXANDER
; TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: P50629C1
; CURRENT APPLICATION NUMBER: US/10/223,880
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-223-880-12

Query Match   78.3%; Score 503; DB 14; Length 110;
Best Local Similarity   85.1%; Pred. No. 5.8e-39;
Matches 97; Conservative 6; Mismatches 5; Indels 6; Gaps 2;

```
Qy   3 QLVQSGAEVKKPGASVKISCKVSGYAFTNYNMHWVRQAPGKGLEWIGYIDPYYGDPGYSQ  62
        |||||| ||||||||||| ||| ||| |||||||||||| ||||| |  |  |  | :|
Db   1 QLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPGNGFTSYNQ  60

Qy  63 KFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARR--GNFPYYFDYWGQGTL 114
        ||||||||||||||||||||||||||||||||||||    | :| |  |||||
Db  61 KFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARQNYGSFA----YWGQGTL 110
```

RESULT 8
US-10-160-232-95
Sequence 95, Application US/10160232
Publication No. US2003008075A1
GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/10/160,232
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 95
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-10-160-232-95

Query Match   76.6%; Score 492; DB 14; Length 136;
Best Local Similarity   78.2%; Pred. No. 7.5e-38;
Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

```
Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMHWVRQAPGKGLEWIGYIDPYYGDPGY  60
         |||||| ||||||||||| ||| ||| |||||||||||| ||||| |  |  |  |
Db  20 QVQLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAPGQGLEWMGAIFPGNGFTSY  79

Qy  61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
        :|||:|  ||||||||||| | | |||||||||| :||||||||||||||||||||||
Db  80 NQKFKGRVTITVDKSTSTAYMQLRSLRSEDTAVYFCARDGD--YYFDYWGQGTLVTVSS 136
```

RESULT 9
US-09-249-011A-6
Sequence 6, Application US/09249011A
Patent No. US20020176855A1
GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.

; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanized
; OTHER INFORMATION: murine anti-human B7-2 heavy chain
US-09-249-011A-6

Query Match   76.4%;   Score 490.5; DB 9; Length 135;
Best Local Similarity 78.2%; Pred. No. 1e-37;
Matches 93; Conservative 11; Mismatches 12; Indels 3; Gaps 1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
Db   20 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAPGQGLEWIGVINIYYDNTNY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
Db   80 NQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA---WYMDYWGQGTLVTVSS 135

RESULT 10
US-09-249-011A-24
; Sequence 24, Application US/09249011A
; Patent No. US2002017685SA1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 24
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Mus sp.

Query Match   76.4%;   Score 490.5; DB 9; Length 461;
Best Local Similarity 78.2%; Pred. No. 3.7e-37;
Matches 93; Conservative 11; Mismatches 12; Indels 3; Gaps 1;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
Db   20 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAPGQGLEWIGVINIYYDNTNY 79

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
Db   80 NQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAA---WYMDYWGQGTLVTVSS 135

RESULT 11
US-10-389-155-16

; Sequence 16, Application US/10389155
; Publication No. US20030229208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Co, Man Sung
;   Schneider, William P.
;   Landolfi, Nicholas F.
;   Coelingh, Kathleen L.
;   Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,155
; FILING DATE: 13-Mar-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-00265OUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-389-155-16

Query Match   76.1%;   Score 488.5; DB 14; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPYNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
Db   61 NQKFKGKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

RESULT 12
US-10-389-417-16
; Sequence 16, Application US/10389417
; Publication No. US20040049014A1

GENERAL INFORMATION:
;   APPLICANT: Queen, Cary L.
;   Co, Man Sung
;   Schneider, William P.
;   Landolfi, Nicholas P.
;   Coelingh, Kathleen L.
;   Selick, Harold E.
;   TITLE OF INVENTION: Improved Humanized Immunoglobulins
;   NUMBER OF SEQUENCES: 100
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/389,417
;   FILING DATE: 13-Mar-2003
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/325,000
;   FILING DATE: 01-JUN-1999
;   APPLICATION NUMBER: US 07/290,975
;   FILING DATE: 28-DEC-1988
;   APPLICATION NUMBER: US 07/310,252
;   FILING DATE: 19-DEC-1990
;   APPLICATION NUMBER: US 08/484,537
;   FILING DATE: 07-JUN-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, William M.
;   REGISTRATION NUMBER: 30,223
;   REFERENCE/DOCKET NUMBER: 011823-00265OUS
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 116 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-389-417-16

Query Match   76.1%; Score 488.5; DB 15; Length 116;
Best Local Similarity   79.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              :||||||||||||||||||||||:||::|||:||:::||||||:||||||||||:|||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              :||||:||||||||:|:|::|||||||||||||||||||||| ||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

APPLICANT: Queen, Cary
;   Co, Man Sung
;   Schneider, William
;   Landolfi, Nicholas
;   Coelingh, Kathleen
;   Selick, Harold
;   TITLE OF INVENTION: Improved Humanized Immunoglobulins
;   FILE REFERENCE: 05882.0078.CNUS01
;   CURRENT APPLICATION NUMBER: US/10/452,357
;   CURRENT FILING DATE: 2003-05-30
;   PRIOR APPLICATION NUMBER: 09/718,993
;   PRIOR FILING DATE: 2000-11-22
;   PRIOR APPLICATION NUMBER: 09/487,200
;   PRIOR FILING DATE: 1995-06-07
;   PRIOR APPLICATION NUMBER: 07/634,278
;   PRIOR FILING DATE: 1990-12-19
;   PRIOR APPLICATION NUMBER: 07/590,275
;   PRIOR FILING DATE: 1990-09-28
;   PRIOR APPLICATION NUMBER: 07/310,252
;   PRIOR FILING DATE: 1989-02-13
;   PRIOR APPLICATION NUMBER: 07/290,975
;   PRIOR FILING DATE: 1988-12-28
;   NUMBER OF SEQ ID NOS: 113
;   SOFTWARE: Patentin version 3.2
SEQ ID NO 57
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: humanized M195 heavy chain antibody

US-10-452-357-57

Query Match   76.1%; Score 488.5; DB 15; Length 116;
Best Local Similarity   79.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              :||||||||||||||||||||||:||::|||:||:::||||||:||||||||||:|||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              :||||:||||||||:|:|::|||||||||||||||||||||| ||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

RESULT 14
US-10-148-844-43
; Sequence 43, Application US/10148844
; Publication No. US20030096403A1
; GENERAL INFORMATION:
;   APPLICANT: Hyo-Jeong Hong
;   Keun-Soo Kim
;   TITLE OF INVENTION: A HUMANIZED ANTIBODY TO SURFACE ANTIGEN S OF HEPATITIS B
;   VIRUS AND A PREPARING METHOD THEREOF
;   FILE REFERENCE: 118.15-US-WO
;   CURRENT APPLICATION NUMBER: US/10/148,844
;   CURRENT FILING DATE: 2002-06-03
;   PRIOR APPLICATION NUMBER: 2000-57891
;   PRIOR FILING DATE: 2000-10-02
;   PRIOR APPLICATION NUMBER: KR 2001-60966
;   PRIOR FILING DATE: 2001-09-29
;   NUMBER OF SEQ ID NOS: 52
;   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Homo sapiens HzS-III-VH

US-10-148-844-43

Query Match   75.8%; Score 486.5; DB 14; Length 118;
Best Local Similarity   77.9%; Pred. No. 2.1e-37;
Matches 95; Conservative 7; Mismatches 13; Indels 7; Gaps 2;

Qy   1 EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              :||||||||||||||||||||||:||::|||:||:::||||||:||||||||||:|||||
Db   1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYPNGGTGY 60

Qy   61 SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              :||||:||||||||:|:|::||||||||||||||||||||| ||||||||||||
Db   61 NQKFKSKATITADESTNTAYMELSSLRSEDTAVYYCAR--GRP-AMDYWGQGTLVTVSS 116

RESULT 13
US-10-452-357-57
; Sequence 57, Application US/10452357
; Publication No. US20040058414A1
; GENERAL INFORMATION:

```
Qy      1  EVQLVQSGAEVKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||||:||:||||||||||||| |||||||||||||||||||
Db      1  EVQLVQSGAEVKKPGASVKVSCKASGYTFTDINVQWVRQAPGKSLEWMGYIYPYSGGTGY 60

Qy     61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFD---YWGQGTLVTV 117
              :||:|||||||||||:||||||||||||||||||||||        ||||||||||||
Db     61  SQKPQGRVTLTVDNSASTAYMELSSLRSEDTAVYYCARN----YGYDSSAYWGQGTLVTV 116

Qy    118  SS 119
              ||
Db    117  SS 118
```

```
RESULT 15
US-10-127-890-169
; Sequence 169, Application US/10127890
; Publication No. US20030166196A1
;  GENERAL INFORMATION:
;
;   APPLICANT: Better, Marc D.
;             Carroll, Stephen F.
;             Studnicka, Gary M.
;
;   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                       Proteins
;
;   NUMBER OF SEQUENCES: 173
;
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;     STREET: 500 West Madison Street, 34th floor
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60661
;
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/127,890
;     FILING DATE: 23-Apr-2002
;     CLASSIFICATION: <Unknown>
;
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/646,360
;     FILING DATE: 13-MAY-1996
;     APPLICATION NUMBER: PCT/US94/05348
;     FILING DATE: 12-MAY-1994
;     APPLICATION NUMBER: US 08/064,691
;     FILING DATE: 12-MAY-1993
;     APPLICATION NUMBER: US 07/988,430
;     FILING DATE: 09-DEC-1992
;     APPLICATION NUMBER: US 07/901,707
;     FILING DATE: 19-JUN-1992
;     APPLICATION NUMBER: US 07/787,567
;     FILING DATE: 04-NOV-1991
;
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McNicholas, Janet M.
;     REGISTRATION NUMBER: 32,918
;     REFERENCE/DOCKET NUMBER: 200-70.P4
;
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/707-8889
;     TELEFAX: 312/707-9155
;     TELEX: 650 388-1248
;
;   INFORMATION FOR SEQ ID NO: 169:
;
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 116 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;
;     SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-10-127-890-169

Query Match             75.3%;  Score 483.5; DB 14;  Length 116;
Best Local Similarity   77.3%;  Pred. No. 3.9e-37;
  Matches   92;  Conservative   11;  Mismatches  13;  Indels   3;  Gaps   1;
```

```
Qy      1  EVQLVQSGAEVKPGASVKISCKVSGYAFTNYNMYWVRQAPGKGLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||||:||:||:|| |||||||||||||||||||||:| |
Db      1  QVQLVQSGAEVKKPGASVKVSCKASGYTFTISYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60

Qy     61  SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTLVTVSS 119
              :|||||||||||||:||||||||||||||||||||||         |||||||||||||
Db     61  NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGG---VFDYWGQGTLVTVSS 116
```

Search completed: December 29, 2004, 18:42:00
Job time : 68.8024 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 29, 2004, 17:37:57 ; Search time 75.6047 seconds
                       (without alignments)
                       521.928 Million cell updates/sec

Title: US-10-774-076-5
Perfect Score: 576
Sequence: 1 QAVVTQESALTTSPGETVTL........ALMYSNHWVFGGGTKLTVLG 110
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
                       2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_23Sep04:*
        1: geneseqp1980s:*
        2: geneseqp1990s:*
        3: geneseqp2000s:*
        4: geneseqp2001s:*
        5: geneseqp2002s:*
        6: geneseqp2003as:*
        7: geneseqp2003bs:*
        8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	559	97.0	112	2	AAR88720	Mouse ant
2	559	97.0	269	2	AAR54756	Murine im
3	559	97.0	415	2	AAR54756	ScFv pRAS
4	556	96.5	269	2	AAR56482	ScFv pRAS
5	555	96.4	131	2	AAR09422	Br-3 Ligh
6	555	96.4	131	2	AAR09422	MAb Br-3
7	555	96.4	131	2	AAW06211	Mouse Br-
8	555	96.4	131	6	AAW85058	Mouse ant
9	555	96.4	114	7	ABU58892	Murine im
10	553	96.0	128	2	ADM07541	3G3 varia
11	550	95.5	112	2	AAR95949	SM3 light
12	548	95.1	261	3	AAY44990	Murine an
13	547	95.0	229	7	ADM07542	Murine im
14	547	95.0	229	7	ADM07544	Murine im
15	547	95.0	230	7	ADM07543	Murine im
16	546	94.8	214	2	AAW27091	Mouse mon
17	546	94.8	256	2	AAR22568	ScFvB18 c
18	546	94.8	256	2	AAR22582	ScFvB18 c
19	546	94.8	428	2	AAW24027	Single ch
20	546	94.8	443	2	AAW24025	Single ch
21	545	94.6	402	2	AAR56485	ScFv pRAS
22	542	94.1	256	2	AAR22584	ScFvB18 c
23	541	93.9	110	2	AAR05038	Metal che
24	541	93.9	110	2	AAR54136	CHA255 li
25	541	93.9	272	7	ADE29203	Multivale
26	541	93.9	273	4	AAB70763	Single ch
27	540	93.8	256	2	AAr22587	ScFvB18 c
28	540	93.8	256	2	AAr22585	ScFvB18 c
29	539	93.6	256	2	AAr22586	ScFv pRAS
30	538	93.4	435	2	AAR56483	ScFV pRAS
31	536	93.1	256	2	AAr22583	ScFvB18 c
32	533	92.5	110	2	AAr04938	Chelate-s
33	530.5	92.1	109	5	AAE17792	Escherich
34	530	92.0	108	7	ADM93152	Murine an
35	528	91.7	110	2	AAr28435	Sequence
36	524	91.0	218	4	AAb20359	Anti-chel
37	522	90.6	391	6	ABR83649	TS1 VL ch
38	519	90.1	129	6	ABU08928	Mouse amy
39	519	90.1	135	4	AAb20356	Anti-chel
40	519	90.1	218	4	AAb20360	Anti-chel
41	517	89.8	109	2	AAW39797	Variable
42	517	89.8	120	4	AAb98667	Murine pr
43	515	89.4	218	4	AAb20358	Anti-chel
44	514	89.2	240	1	AAP80157	Biosynthe
45	513	89.1	109	2	AAW39798	Variable

ALIGNMENTS

RESULT 1
AAR88720
ID   AAR88720 standard; protein; 112 AA.
XX
AC   AAR88720;
XX
DT   26-SEP-1996 (first entry)
XX
DE   Mouse antibody lambda chain variable region consensus sequence.
XX
KW   Antibody; stability; instability; mutagenesis; amino acid frequency;
KW   canonical sequence approximation; substitution; immunoglobulin;
KW   light chain; variable region; VL-region; diagnosis; immunoassay;
KW   cancer treatment; autoimmune disease; immunotoxin; improved yield.
XX
OS   Mus musculus.
XX
PN   DB4425115-A1.
XX
PD   18-JAN-1996.
XX
PF   15-JUL-1994; 94DE-04425115.
XX
PR   15-JUL-1994; 94DE-04425115.
XX
PA   (BOEF) BOEHRINGER MANNHEIM GMBH.
XX
PI   Steipe B, Steinbacher S;
XX
DR   WPI; 1996-069594/08.
XX
PT   Functional antibodies modified to increase or decrease stability - have
PT   specific amino acid substns. in the variable domain, determined by
PT   reference to consensus sequences.
PS   Claim 2; Page 35; 43pp; German.
XX
CC   Consensus sequences were established for antibody variable regions from
CC   human and mouse heavy and light (kappa and lambda) chains. In addition,
CC   frequency tables listing the amino acids which can be found at each
CC   position were compiled. In a new method, mutations are introduced into an
CC   antibody variable domain by reference to the frequency table. When an
CC   amino acid is replaced by one which occurs at a higher frequency at that
CC   position, the resulting antibody chain is more stable than the wild-type;
CC   when an amino acid is replaced by one which occurs less frequently (or
CC   not at all), the resulting antibody is less stable than the wild-type.
CC   Stabilised antibodies are useful as diagnostic reagents, as catalysts and
CC   in treatment of cancer, autoimmune diseases and infections. Destabilised

```
CC   antibodies have improved (faster) pharmacokinetic properties. The present
CC   sequence is the mouse lambda light chain variable region consensus
CC   sequence.
XX
SQ   Sequence 112 AA;

Query Match             97.0%;  Score 559;  DB 2;  Length 112;
Best Local Similarity   97.3%;  Pred. No. 1.2e-39;
Matches  107;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
        |||||||||||||||||||||||||||||||| ||||||||||||||||| |||  |||
Db   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV  60

Qy  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
```

RESULT 2

```
ID   AAR54756 standard; protein; 269 AA.
XX
AC   AAR54756;
XX
DT   25-MAR-2003 (revised)
DT   06-DEC-1994 (first entry)
XX
DE   pRAS111 between HindIII and EcoRI sites.
XX
KW   Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus; Penton fibre;
KW   Ad5; Fusion sites; PCR; polymerase chain reaction.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FH
FT   Protein         1..269
FT                   /label= Single chain Fv fragment
FT   Peptide         1..22
FT                   /label= pelB leader peptide
FT   Protein         23..142
FT                   /label= heavy chain variable region
FT   Region          23..51
FT                   /label= VH FR1
FT   Region          52..57
FT                   /label= VH CDR 1
FT   Region          58..71
FT                   /label= VH FR2
FT   Region          72..88
FT                   /label= VH CDR 2
FT   Region          89..120
FT                   /label= VH FR3
FT   Region          121..131
FT                   /label= VH CDR 3
FT   Region          132..142
FT                   /label= VH FR4
FT   Peptide         143..265
FT                   /label= (G4S)3 Linker
FT   Protein         158..269
FT                   /label= Light chain variable region
FT   Region          158..179
FT                   /label= VL FR1
FT   Region          180..193
FT                   /label= VL CDR 1
FT   Region          194..207
FT                   /label= VL FR2
FT   Region          208..215
FT                   /label= VL CDR 2
FT   Region          216..247
FT                   /label= VL FR3
FT   Region          248..256
FT                   /label= VL CDR 3
FT   Region          257..269
FT                   /label= VL FR3
```

```
PN   WO9410323-A1.                          /label= VL FR3
XX
PD   11-MAY-1994.
XX
PF   04-NOV-1993;  93WO-GB002267.
XX
PR   04-NOV-1992;  92GB-00023084.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI   Spooner RA,  Epenetos AA;
XX
PT   Virus with modified binding moiety specific for the target cells - used
PT   to deliver genes for gene therapy and cancer treatment.
XX
PS   Example 2; Page 69-70; 110pp; English.
XX
CC   AAR54756 showes an ScFv (VH and VL partner domains are linked via a
CC   flexible oligopeptide) between the HindIII and EcoRI sites of pRAS111.
CC   The 130 bp HindIII-PstI fragment of pRAS117 (AAQ64806) was used to
CC   replace the corresponding fragment of pRAS111 (AAQ64817), to generate
CC   pRAS118. This generates a NIP-reactive ScFv (NIP = 4-hydroxyl-3-iodo-5-
CC   nitrophylacetic acid) with a BglII cloning site immediately downstream of
CC   the pelB leader, suitable for inserting fragments of Ad5 fibre. The
CC   invention is concerned with the fusion of an ScFv with the Ad5 fibre such
CC   that the fusion sequence can be used to target cells for gene therapy.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 269 AA;
```

RESULT 3

```
ID   AAR56484 standard; protein; 415 AA.
XX
AC   AAR56484;
XX
DT   25-MAR-2003 (revised)
DT   26-MAR-1995 (first entry)
XX
DE   ScFv pRAS109 and pRAS113.
XX
KW   Amplification; single chain variable region fusion protein; PCR.
XX
OS   Synthetic.
XX
PN   WO9415644-A1.
XX
PD   21-JUL-1994.
XX
PF   17-JAN-1994;  94WO-GB000087.
XX
PR   15-JAN-1993;  93GB-00000686.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
```

```
Query Match             97.0%;  Score 559;  DB 2;  Length 269;
Best Local Similarity   97.3%;  Pred. No. 3.2e-39;
Matches  107;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV   60
         |||||||||||||||||||||||||||||||| ||||||||||||||||| |||  |||
Db  158  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV  217

Qy   61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  218  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  267
```

```
PI   Epenetos AA, Spooner RA, Deonarain M;
XX
DR   WPI; 1994-248907/30.
DR   N-PSDB; AAQ70660.
XX
PT   cells.
PT   esp. for treating mammals for destroying target cells, tumour
PT   New cpds. comprising a targeting portion and a cytotoxic portion - used
XX
PS   Disclosure; Fig 10; 114pp; English.
XX
CC   correct PN field.)
CC   EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to
CC   The sequence is that of the ScFv pRAS109 and pRAS113 between HindIII and
XX
SQ   Sequence 415 AA;

Qy   Query Match      97.0%;  Score 559;  DB 2;  Length 415;
     Best Local Similarity   97.3%;  Pred. No. 5e-39;
     Matches  107;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy     1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSAANWVQEKPDHLFTGLIGGTINRVPGV 60
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||| |||
Db   158 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRRAPGV 217

Qy    61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   218 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 267
```

RESULT 4
```
ID   AAR56482 standard; protein; 269 AA.
XX
AC   AAR56482;
XX
DT   25-MAR-2003  (revised)
DT   26-MAR-1995  (first entry)
XX
DE   ScFv pRAS107 and pRAS111.
XX
KW   Amplification; single chain variable region fusion protein; PCR.
XX
OS   Synthetic.
XX
PN   WO9415644-A1.
XX
PD   21-JUL-1994.
XX
PF   17-JAN-1994;  94WO-GB000087.
XX
PR   15-JAN-1993;  93GB-00000686.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI   Epenetos AA, Spooner RA, Deonarain M;
XX
DR   WPI; 1994-248907/30.
DR   N-PSDB; AAQ56482.
XX
PT   New cpds. comprising a targeting portion and a cytotoxic portion - used
PT   esp. for treating mammals for destroying target cells, partic. tumour
PT   cells.
XX
PS   Disclosure; Fig 4; 114pp; English.
XX
CC   The sequence is that of the ScFv pRAS107 and pRAS111 between HindIII and
CC   EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 269 AA;

Qy   Query Match      96.5%;  Score 556;  DB 2;  Length 269;
     Best Local Similarity   96.4%;  Pred. No. 5.7e-39;
     Matches  106;  Conservative  1;  Mismatches  3;  Indels  0;  Gaps  0;

Qy     1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSAANWVQEKPDHLFTGLIGGTINRVPGV 60
         ||||||||||||||||||||||||||||||||| :|||||||||||||||||||||| |||
Db   158 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRRAPGV 217

Qy    61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   218 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 267
```

RESULT 5
```
ID   AAR09422 standard; protein; 131 AA.
XX
AC   AAR09422;
XX
DT   25-MAR-2003  (revised)
DT   04-MAR-1993  (first entry)
XX
DE   Br-3 Light Chain V Region (mouse).
XX
KW   Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
KW   antigen; diagnosis; cancer; tumour.
XX
OS   Mus musculus.
XX
PN   WO9002569-A.
XX
PD   22-MAR-1990.
XX
PF   08-SEP-1988;  88US-00241744.
XX
PR   08-SEP-1988;  88US-00241744.
PR   13-SEP-1988;  88US-00243739.
PR   04-OCT-1988;  88US-00253002.
PR   19-JUN-1989;  89US-00367641.
PR   21-JUL-1989;  89US-00382768.
XX
PA   (ITGB-) INT GENETIC ENG INC.
PA   (INGB-) INGENE INT GENETIC.
XX
PI   Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX
DR   WPI; 1990-1158251/15.
DR   N-PSDB; AAQ08604.
XX
PT   Chimeric mouse-human antibodies - prepd. using genes coding for constant
PT   human region murine variable region, esp. to 3 tumour antigen.
XX
PS   Claim 13; Page 123 + Fig 14; 173pp; English.
XX
CC   The sequence is used in the prodn. of a chimeric antibody mol. comprising
CC   two light chains and two heavy chains, each having a constant region
CC   (human) and a variable region (murine) having specificity to an antigen
CC   bound by murine monoclonal antibody (MAb) Br-3. The chimeric antibodies
CC   can be used for any purpose for which the original murine MAbs can be
CC   used, with the advantage that they are more compatible with the human
CC   body. They are esp. used for the diagnosis and treatment of cancer.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 131 AA;

Qy   Query Match      96.4%;  Score 555;  DB 2;  Length 131;
     Best Local Similarity   96.4%;  Pred. No. 3.2e-39;
     Matches  106;  Conservative  0;  Mismatches  4;  Indels  0;  Gaps  0;

Qy     1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRVPGV 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRRAPGV 79

Qy    61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
```

Mon Jan 3 13:38:52 2005
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Page 4

Left column (RESULT 6):

```
Db          80 PARFSGGSLIGDKAALTITGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 129
               ||||||||||||||||||||||||||||||||||||||||||||||||||
            80 PARFSGGSLIGDKAALTITGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 129

RESULT 6

ID   AAW06211 standard; protein; 131 AA.
XX
AC   AAW06211;
XX
DT   25-MAR-2003  (revised)
DT   12-FEB-1997  (first entry)
XX
DE   MAb Br-3 light chain variable region.
XX
KW   Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
KW   tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma;
KW   ovary carcinoma; cancer; diagnosis; therapy; light chain.
XX
OS   Mus sp.
XX
PN   US576184-A.
XX
PD   19-NOV-1996.
XX
PF   27-DEC-1994;  94US-00364001.
XX
PR   06-SEP-1988;  88US-00240624.
PR   08-SEP-1988;  88US-00241744.
PR   13-SEP-1988;  88US-00243739.
PR   04-OCT-1988;  88US-00253002.
PR   19-JUN-1989;  89US-00367641.
PR   21-JUL-1989;  89US-00382768.
PR   06-MAY-1991;  91US-00659401.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;
XX
DR   WPI; 1997-011249/01.
DR   N-PSDB; AAT43436.
XX
PT   Chimeric mouse-human antibodies - recognise a human tumour antigen, used
PT   for the treatment and diagnosis of human cancers.
XX
PS   Example 3; Fig 14; 102pp; English.
XX
CC   The light chain variable region (AAW06211) of mouse monoclonal antibody
CC   Br-3 is the product of a cDNA clone (AAT43436) isolated from a Br-3
CC   hybridoma cDNA library. MAb Br-3 (IgG1) binds to an antigen that is
CC   expressed on the surface of human lung, breast, colon and ovary
CC   carcinomas, but not on most normal adult tissues. The light chain and
CC   heavy chain variable regions (see also AAW06212) of B38-1 can be linked
CC   to human constant regions and expressed in transformed host cells. Novel
CC   mouse-human chimeric antibodies (see also AAW06209-10 and AAW06213-18)
CC   can be produced that have specificity to human tumour antigens and can be
CC   used for the treatment and diagnosis of human cancer. (Updated on 25-MAR-
CC   2003 to correct PF field.)
XX
SQ   Sequence 131 AA;

Query Match             96.4%;  Score 555;  DB 2;  Length 131;
Best Local Similarity   96.4%;
Matches  106;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps   0;

Qy            1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTNNRAPGV 60
                |||||||||||||||||||||||||||||||||||||||||| || ||||||| ||| ||
Db           20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 79

Qy           61 PARFSGGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
                ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db           80 PARFSGGSLIGDKAALTITGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 129
```

Right column (RESULT 7):

```
RESULT 7

ID   AAW85058 standard; protein; 131 AA.
XX
AC   AAW85058;
XX
DT   20-MAR-2003  (revised)
DT   16-APR-1999  (first entry)
XX
DE   Mouse Br-3 heavy chain variable region.
XX
KW   Heavy chain variable region; murine antibody Br-3; antibody ING-1;
KW   chimeric immunoglobulin; human tumour antigen; chimeric antibody;
KW   treatment; human cancer.
XX
OS   Mus sp.
XX
PN   US5843685-A.
XX
PD   01-DEC-1998.
XX
PF   06-JUN-1995;  95US-00466034.
XX
PR   06-SEP-1988;  88US-00240624.
PR   08-SEP-1988;  88US-00241744.
PR   13-SEP-1988;  88US-00243739.
PR   04-OCT-1988;  88US-00253002.
PR   19-JUN-1989;  89US-00367641.
PR   21-JUL-1989;  89US-00382768.
PR   06-SEP-1989;  89WO-US003852.
PR   06-MAY-1991;  91US-00659401.
PR   27-DEC-1994;  94US-00364001.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;
XX
DR   WPI; 1999-044574/04.
DR   N-PSDB; AAV71154.
XX
PT   Chimeric antibody specific for human tumour antigen - useful as
PT   immunoassay, imaging or antitumour agent.
XX
PS   Example 3; Fig 14; 92pp; English.
XX
CC   The present sequence represents the heavy chain variable region of murine
CC   antibody Br-3. The sequence was used to create chimeric mouse-human
CC   immunoglobulins which recognise the human tumour antigen bound by
CC   antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The
CC   chimeric antibodies also have an antigen-binding site that competitively
CC   inhibits the binding of antibody ING-1, and mediate complement-dependent
CC   cytolysis of target cells or antibody-dependent cellular cytotoxicity to
CC   target cells. The chimeric antibodies can be used for therapeutic
CC   purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 131 AA;

Query Match             96.4%;  Score 555;  DB 2;  Length 131;
Best Local Similarity   96.4%;
Matches  106;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps   0;

Qy            1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTNNRAPGV 60
                |||||||||||||||||||||||||||||||||||||||||| || ||||||| ||| ||
Db           20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 79

Qy           61 PARFSGGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
                ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db           80 PARFSGGSLIGDKAALTITGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 129

RESULT 8
```

```
ID   ABU58892 standard; protein; 131 AA.
XX
AC   ABU58892;
XX
DT   16-APR-2003  (first entry)
XX
DE   Mouse antibody light chain variable region #2.
XX
KW   Mouse; human tumour antigen; anti-human tumour antigen-antibody;
KW   ING-1 antibody; cell line HB9812; immunoassay; imaging; tumour diagnosis;
KW   tumour therapy; cytostatic; light chain variable region.
XX
OS   Mus sp.
XX
XX
PN   US6461824-B1.
XX
PD   08-OCT-2002.
XX
PF   06-JUN-1995;  95US-00467142.
XX
PR   06-SEP-1988;  88US-00240624.
PR   08-SEP-1988;  88US-00241744.
PR   13-SEP-1988;  88US-00243739.
PR   04-OCT-1988;  88US-00253002.
PR   19-JUN-1989;  89US-00367641.
PR   21-JUL-1989;  89US-00382768.
PR   06-SEP-1989;  89WO-US003852.
PR   06-MAY-1991;  91US-00659401.
PR   27-DEC-1994;  94US-00364001.
XX
PA   (XOMA ) XOMA TECHNOLOGY LTD.
XX
PI   Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX
DR   WPI; 2003-196707/19.
DR   N-PSDB; ABK79229.
XX
PT   Antibody for detecting antigen in animal or killing cells carrying
PT   antigen comprises human constant region and variable region having
PT   specificity for human tumor antigen bound by ING-1 antibody.
XX
PS   Example 3; Fig 14; 101pp; English.
XX
CC   The invention describes an antibody comprising a human constant region
CC   and a variable region having specificity for the human tumour antigen
CC   bound by the ING-1 antibody, where the ING-1 is produced by cell line
CC   HB9812 as deposited with ATCC, and the antibody has the same affinity as
CC   the ING-1 for the human tumour antigen. The antibody is useful in an
CC   immunoassay method for detecting an antigen in a sample by contacting a
CC   label-detectable antigen in the sample with the antibody, detecting the
CC   label and relating the detected label to the presence of the antigen; for
CC   use in an imaging method for revealing the presence of a label-detectable
CC   antigen in an animal by contacting the antibody with a part of the animal
CC   suspected of containing the antigen, detecting the label and relating the
CC   detected label to the presence of the antigen; and for killing cells
CC   carrying an antigen by contacting the cells with the antibody and
CC   allowing the killing to occur. The antibodies are useful in tumour
CC   diagnosis and therapy. The chimeric antibodies bind to the surface of
CC   human tumour cells but do not bind detectably to normal cells, e.g.,
CC   fibroblasts, endothelial cells or epithelial cells in the major organs.
CC   The high biological activity of the chimeric antibodies against human
CC   tumour cell lines combined with minimal reactivity with normal tissues
CC   imply that these antibodies may mediate selective destruction of
CC   malignant tissue. The presence of human rather than murine antigenic
CC   determinants on the chimeric antibodies increases their resistance to
CC   rapid clearance from the body relative to the original murine mAbs. This
CC   resistance to clearance enhances the potential utility of these chimeric
CC   antibodies, as well as their derivatives, in tumour diagnosis and
CC   therapy. This is the amino acid sequence of a mouse antibody light chain
CC   variable region used in the creation of an anti-human tumour antigen-
CC   antibody
XX
SQ   Sequence 131 AA;

  Query Match             96.4%;  Score 555;  DB 6;  Length 131;
  Best Local Similarity   96.4%;  Pred. No. 3.2e-39;
  Matches 106;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 79

Qy         61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 PARFSGSLIGDKAALTITGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 129


RESULT 9
ADM07541

ID   ADM07541 standard; protein; 114 AA.
XX
AC   ADM07541;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Murine immunoglobulin 15A2 light chain variable domain protein.
XX
KW   murine; mouse; heavy; immunoglobulin;
KW   antibody light chain variable domain; antiallergic; allergy; IgE;
KW   gene therapy; 15A2.
XX
OS   Mus sp.
XX
XX
PN   WO2003060080-A2.
XX
PD   24-JUL-2003.
XX
PF   20-DEC-2002;  2002WO-US041562.
XX
PR   21-DEC-2001;  2001US-0344874P.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR   WPI; 2003-598521/56.
XX
PT   New canine heavy and light chain variable domain polypeptides, useful for
PT   treating canine allergy.
XX
PS   Example 5; Fig 2; 130pp; English.
XX
CC   The invention relates to a novel canine heavy or light chain variable
CC   domain polypeptide. The protein of the invention demonstrates
CC   antiallergic activity and may be useful for treating canine allergy,
CC   possibly via gene therapy. The current sequence is that of a murine
CC   immunoglobulin light chain variable domain protein of the invention.
XX
SQ   Sequence 114 AA;

  Query Match             96.0%;  Score 553;  DB 7;  Length 114;
  Best Local Similarity   96.4%;  Pred. No. 4e-39;
  Matches 106;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGPNNRAPGV 63

Qy         61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVRGGGTKLTVLG 110
              ||||||||||||||||||||||||||||||||||||||||| ||||||||
Db         64 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 113


RESULT 10
AAR95949
```

```
ID   AAR95949 standard; protein; 128 AA.
XX
AC   AAR95949;
XX
DT   11-FEB-1997  (first entry)
XX
DE   3G3 variable lambda chain.
XX
KW   Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse;
KW   F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
KW   chimeric antibody; isotype-switched antibody; therapy; infection; human;
KW   pneumonia; bronchiolitis; animal.
XX
OS   Mus musculus.
XX
PN   WO9616974-A1.
XX
PD   06-JUN-1996.
XX
PF   01-DEC-1995;   95WO-US015716.
XX
PR   01-DEC-1994;   94US-0034 8548.
XX
PA   (ORAV-) ORAVAX INC.
XX
PI   Berdoz J, Kraehenbuhl J;
XX
DR   WPI; 1996-286826/29.
DR   N-PSDB; AAT30559.
XX
PT   DNA encoding variable region of antibody HNK-20 - for treating
PT   respiratory syncytial virus infection.
XX
PS   Example; Page 29; 75pp; English.
XX
CC   This sequence represents the variable lambda chain of an antibody
CC   produced by the 3G3 hybridoma cell line. AAR95946-R95948 represent
CC   sequences for variable regions of an antibody produced by the hybridoma
CC   cell line HNK-20. HNK-20 and 3G3 are murine hybridoma cell lines, that
CC   produces IgA specific for the F glycoprotein of respiratory syncytial
CC   virus (RSV). The DNA encoding these sequences were isolated using primers
CC   specific for the 5' untranslated region of the variable region, and for
CC   the intron downstream of the rearranged J region (see AAT30459-T30545 for
CC   primer sequences). The DNA encoding these sequences can be inserted into
CC   vectors containing heterologous (such as human) constant region genes,
CC   for the production of chimeric and isotype-switched antibodies. The
CC   antibodies are useful in the treatment and diagnosis of infection by RSV,
CC   such as pneumonia and bronchiolitis, in humans and animals. By using
CC   genomic DNA as a template, variable region genes can be isolated without
CC   producing fragments that have to be adapted for recombinant antibody
CC   expression. Also, by using the genomic DNA, no knowledge of the DNA
CC   sequence encoding the target variable region is required. Chimeric
CC   antibodies produced from these proteins, that contain the constant region
CC   of the host being treated, are less likely to cause adverse immune
CC   reactions
XX
SQ   Sequence 128 AA;

  Query Match          96.0%;  Score 553;  DB 2;  Length 128;
  Best Local Similarity  97.2%;  Pred. No. 4.6e-39;
  Matches 106;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy          1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db         20  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRAPGV 79

Qy         61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db         80  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 128
```

```
ID   AAY03868 standard; protein; 112 AA.
XX
AC   AAY03868;
XX
DT   16-JUN-1999  (first entry)
XX
DE   SM3 light chain variable region.
XX
KW   SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy;
KW   immune response; arthritis; multiple sclerosis; asthma; diabetes;
KW   inflammatory disorder; transplant rejection; graft versus host disease.
XX
OS   Unidentified.
XX
PN   WO9910379-A1.
XX
PD   04-MAR-1999.
XX
PF   24-AUG-1998;   98WO-GB002542.
XX
PR   22-AUG-1997;   97GB-00017946.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI   Freemont PS, Snary D, Sternberg MJE, Bates PA, Dokurno P;
XX
DR   WPI; 1999-204650/17.
DR   N-PSDB; AAX31970.
XX
PT   New SM3 antibody crystal structures - used to develop agents for treating
PT   e.g. tumors, autoimmune disorders, allergies, inflammatory disorders or
PT   transplant rejection.
XX
PS   Disclosure; Page 279; 316pp; English.
XX
CC   The invention relates to a process for preparing a crystal using cadmium.
CC   Structure factors or structural coordinates obtained from the crystal of
CC   SM3 antibody bound to an epitope can be used to design mimics of the
CC   antibody or the epitope. The crystals comprise at least an epitope
CC   binding fragment of the SM3 antibody bound to a peptide recognised by the
CC   epitope binding site of SM3. The products and methods can be used to
CC   develop agents for the detection of tumour cells and for therapy against
CC   tumours. MUC1 epitope mimics can also be used to prevent or decrease an
CC   immune response, e.g. in the therapy of diseases caused by autoimmune
CC   responses (such as arthritis, multiple sclerosis, asthma or diabetes),
CC   allergies, inflammatory disorders or transplant rejections such as graft
CC   versus host disease. The present sequence represents the amino acid
CC   sequence of a light chain variable region of SM3 antibody
XX
SQ   Sequence 112 AA;

  Query Match          95.5%;  Score 550;  DB 2;  Length 112;
  Best Local Similarity  97.2%;  Pred. No. 7.1e-39;
  Matches 105;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy          3  VVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVPA 62
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||| ||||
Db          3  VVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRAPGVPA 62

Qy         63  RFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         63  RFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
```

```
RESULT 11
AAY03868

RESULT 12
AAY44990

ID   AAY44990 standard; protein; 261 AA.
XX
AC   AAY44990;
XX
DT   23-MAY-2000  (first entry)
XX
DE   Murine anti-Lewis Y antibody single-chain Fv fragment.
```

KW   Murine; Lewis Y; LeY; antibody; multifunctional compound; single-chain Fv fragment; scFv;
KW   heterominibody; multifunctional compound; CH1-domain; light chain; constant domain; CL-domain;
KW   heavy chain; constant domain; light chain; CD80 molecule; immunoglobulin;
KW   cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW   antiproliferative; prevention; treatment; malignant; leukaemia; solid tumour; carcinoma; melanoma; sarcoma;
KW   lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   Region   20..128
FT   /label= Immunoglobulin_light_chain_variable_region
FT   Region   144..261
FT   /label= Immunoglobulin_heavy_chain_variable_region
XX
PN   WO200006605-A2.
XX
PD   10-FEB-2000.
XX
PF   28-JUL-1999; 99WO-EP005416.
XX
PR   28-JUL-1998; 98EP-00114082.
XX
PA   (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI   Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR   WPI; 2000-195265/17.
DR   N-PSDB; AA250583.
XX
PS   Claim 8; Fig 6; 166pp; English.
XX
PT   New multifunctional compounds useful for preventing and/or treating
PT   malignant cell growth and for detection and diagnosis.
XX
CC   The patent discloses heterominibodies which are multifunctional compounds
CC   produceable in a mammalian host cell as a secretable and fully functional
CC   heterodimer of two polypeptide chains, where one of the polypeptide
CC   chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC   heavy chain) and the other chain comprises CL-domain (constant domain of
CC   an immunoglobulin light chain). The polypeptide chains further comprise,
CC   fused to the constant domains at least two (poly)peptides having
CC   different receptor or ligand functions, where further at least two of the
CC   different (poly)peptides lack an intrinsic affinity for one another and
CC   are linked via the constant domains. The heterominibodies have
CC   cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC   activities. These compounds can be used for diagnosing, preventing and
CC   treating malignant cell growth related to malignancies of haematopoietic
CC   cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC   melanomas and sarcomas. The present sequence is a murine anti-Lewis Y
CC   antibody single-chain Fv (scFv) fragment which is used in the
CC   construction of heterominibodies comprising CH1 (first constant domain of
CC   human IgG1 heavy chain), CK (constant region of human Ig-kappa light
CC   chain) and CD80 molecule.
XX
SQ   Sequence 261 AA;

Query Match   95.1%; Score 548; DB 3; Length 261;
Best Local Similarity   97.2%; Pred. No. 2.6e-38;
Matches   105; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   3 VVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVPA 62
              ||||||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||
Db   22 VVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRVPGVPA 81

Qy   63 RFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
              ||||||||||||||||||||||||||||||||||||||||||||| ||
Db   82 RFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLEVLG 129

RESULT 13
ADM07542

ID   ADM07542 standard; protein; 229 AA.
XX
AC   ADM07542;
XX
DT   20-MAY-2004 (first entry)
XX
DE   Murine immunoglobulin 15A2/1NGQ light chain variable domain protein.
XX
KW   murine; mouse; heavy; immunoglobulin;
KW   antibody light chain variable domain; antiallergic; allergy; IgE;
KW   gene therapy; 15A2/1NGQ.
XX
OS   Mus sp.
XX
PN   WO2003060080-A2.
XX
PD   24-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-US041362.
XX
PR   21-DEC-2001; 2001US-0344874P.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR   WPI; 2003-598521/56.
XX
PS   Example 6; Fig 5; 130pp; English.
XX
PT   New canine heavy and light chain variable domain polypeptides, useful for
PT   treating canine allergy.
XX
CC   The invention relates to a novel canine heavy or light chain variable
CC   domain polypeptide. The protein of the invention demonstrates
CC   antiallergic activity and may be useful for treating canine allergy,
CC   possibly via gene therapy. The current sequence is that of a murine
CC   immunoglobulin light chain variable domain protein of the invention.
XX
SQ   Sequence 229 AA;

Query Match   95.0%; Score 547; DB 7; Length 229;
Best Local Similarity   96.3%; Pred. No. 2.7e-38;
Matches   105; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              |||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||
Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109

RESULT 14
ADM07544

ID   ADM07544 standard; protein; 229 AA.
XX
AC   ADM07544;
XX
DT   20-MAY-2004 (first entry)
XX
DE   Murine immunoglobulin 15A2/2VIR light chain variable domain protein.
XX
KW   murine; mouse; heavy; immunoglobulin;
KW   antibody light chain variable domain; antiallergic; allergy; IgE;
KW   gene therapy; 15A2/2VIR.
XX
OS   Mus sp.
XX
PN   WO2003060080-A2.
XX
PD   24-JUL-2003.

```
XX
PF   20-DEC-2002; 2002WO-US041362.
XX
PR   21-DEC-2001; 2001US-0344874P.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR   WPI; 2003-598521/56.
XX
     New canine heavy and light chain variable domain polypeptides, useful for
     treating canine allergy.
XX
PS   Example 6; Fig 5; 130pp; English.
XX
PT
XX
CC   The invention relates to a novel canine heavy or light chain variable
CC   domain polypeptide. The protein of the invention demonstrates
CC   antiallergic activity and may be useful for treating canine allergy,
CC   possibly via gene therapy. The current sequence is that of a murine
CC   immunoglobulin light chain variable domain protein of the invention.
XX
SQ   Sequence 229 AA;

Query Match             95.0%;  Score 547;  DB 7;  Length 229;
Best Local Similarity   96.3%;  Pred. No. 2.7e-38;
Matches 105;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||| |||
Db          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGPNNRAPGV 60

Qy         61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
```

```
CC   domain polypeptide. The protein of the invention demonstrates
CC   antiallergic activity and may be useful for treating canine allergy,
CC   possibly via gene therapy. The current sequence is that of a murine
CC   immunoglobulin light chain variable domain protein of the invention.
XX
SQ   Sequence 230 AA;

Query Match             95.0%;  Score 547;  DB 7;  Length 230;
Best Local Similarity   96.3%;  Pred. No. 2.7e-38;
Matches 105;  Conservative   0;  Mismatches   4;  Indels   0;  Gaps   0;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||| |||
Db          2 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGPNNRAPGV 61

Qy         61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 110

Search completed: December 29, 2004, 17:57:32
Job time : 78.6047 secs
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RESULT 15
ID   ADM07543 standard; protein; 230 AA.
XX
AC   ADM07543;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Murine immunoglobulin 15A2/1FBI light chain variable domain protein.
XX
KW   murine; mouse; heavy; immunoglobulin;
KW   antibody light chain variable domain; antiallergic; allergy; IgE;
KW   gene therapy; 15A2/1FBI.
XX
OS   Mus sp.
XX
XX
PN   WO200306080-A2.
XX
PD   24-JUL-2003.
XX
PF   20-DEC-2002; 2002WO-US041362.
XX
PR   21-DEC-2001; 2001US-0344874P.
XX
PA   (IDEX-) IDEXX LAB INC.
XX
PI   Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR   WPI; 2003-598521/56.
XX
     New canine heavy and light chain variable domain polypeptides, useful for
     treating canine allergy.
XX
PS   Example 6; Fig 5; 130pp; English.
XX
PT
XX
CC   The invention relates to a novel canine heavy or light chain variable
```

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OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 ; Search time 75.9292 Seconds
                 (without alignments)
                 833.556 Million cell updates/sec

Title: US-10-774-076-5
Perfect score: 576
Sequence: 1 QAVVTQESALTTSPGETVTL.........ALWYSNHWVFGGGTKLTVLG 110

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_02:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID		Description
1	552	95.8	129	1	LV1D_MOUSE	P01726 mus musculu
2	552	95.8	129	1	LV1E_MOUSE	P01727 mus musculu
3	551	95.7	129	1	LV1B_MOUSE	P01724 mus musculu
4	540	93.8	129	2	Q8VDE2	Q8vde2 mus musculu
5	535.5	93.0	113	2	Q8CGS1	Q8cgs1 mus musculu
6	534	92.7	110	1	LV1C_MOUSE	P01725 mus musculu
7	530.5	92.1	109	2	Q9ET13	Q9et13 mus musculu
8	514	89.2	129	1	LV2B_MOUSE	P01729 mus musculu
9	487	84.5	117	1	LV1A_MOUSE	P01723 mus musculu
10	460	79.9	117	1	LV2A_MOUSE	P01728 mus musculu
11	279	48.4	117	1	LV0A_HUMAN	P04211 homo sapien
11	244.5	42.4	111	1	LV6C_HUMAN	P06317 homo sapien
12	239.5	41.6	107	2	Q9NSD6	Q9nsd6 homo sapien
13	239	41.5	236	2	Q6GMV7	Q6gmv7 homo sapien
14	236.5	41.1	111	1	LV2C_HUMAN	P01706 homo sapien
15	236.5	41.1	237	2	Q8WTK4	Q8wtk4 homo sapien
16	235.5	40.9	237	2	Q8WTU6	Q8wtu6 homo sapien
17	234	40.6	110	1	LV2J_HUMAN	P01713 homo sapien
18	234	40.6	112	2	Q96JD1	Q96jd1 homo sapien
19	234	40.6	233	2	Q8NSF4	Q8nsf4 homo sapien
20	233.5	40.5	248	2	Q7SYU1	Q7syu1 xenopus lae
21	233	40.5	112	1	LV6A_HUMAN	P01721 homo sapien
22	233	40.5	236	2	Q6GMX4	Q6gmx4 homo sapien
23	232	40.3	130	1	LV1G_HUMAN	P06316 homo sapien
24	231.5	40.2	109	1	LV1I_HUMAN	P06888 homo sapien
25	228.5	39.7	233	2	Q6PJA3	Q6pja3 homo sapien
26	228	39.6	233	2	AAH18749	Aah18749 homo sapi
27	228	39.6	108	1	LV3A_HUMAN	P01714 homo sapien
28	227.5	39.5	111	1	LV2D_HUMAN	P01707 homo sapien
29	227.5	39.5	116	2	Q96DD0	Q96dd0 homo sapien
30	227.5	39.5	236	2	Q6IPQ0	Q6ipq0 homo sapien
31	227	39.4	236	2	Q6IPQ0	Q6ipq0 homo sapien
32	226.5	39.3	167	2	BAC05245	Bac05245 homo sapi
33	226.5	39.3	235	2	Q6GMW6	Q6gmw6 homo sapien
34	226	39.2	235	2	Q8NEJ1	Q8nej1 homo sapien
35	225.5	39.1	235	2	Q6PIK1	Q6pik1 homo sapien
36	225.5	39.1	235	2	AAH33102	Aah33102 homo sapi
37	223	38.7	230	2	Q7Z2U3	Q7zzu3 homo sapien
38	223	38.7	236	2	Q96E61	Q96e61 homo sapien
39	222.5	38.6	245	2	Q6GNC5	Q6gnc5 homo sapien
40	222	38.5	236	2	Q6PIQ7	Q6piq7 homo sapien
41	222	38.5	236	2	AAH30983	Aah30983 homo sapi
42	221.5	38.5	111	1	LV2L_HUMAN	P04220 homo sapien
43	220.5	38.3	111	1	LV3B_HUMAN	P80748 homo sapien
44	220.5	38.3	235	2	BAC85358	Bac85358 homo sapi
45	219.5	38.1	233	2	Q8TBC9	Q8tbc9 homo sapien

ALIGNMENTS

RESULT 1
LV1D_MOUSE
ID   LV1D_MOUSE   STANDARD;   PRT;   129 AA.
AC   P01726;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda-1 chain V region H2020 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=79084170; PubMed=103630;
RA   Bernard O., Hozumi N., Tonegawa S.;
RT   "Sequences of mouse immunoglobulin light chain genes before and after
RT   somatic changes.";
RL   Cell 15:1133-1144(1978).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01724; 1A6V.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   129   Ig lambda-1 chain V region H2020.
FT   DOMAIN   20   125   Ig-like.
FT   NON_TER   129   129
SQ   SEQUENCE   129 AA; 13465 MW; A57C8910157C1316 CRC64;

  Query Match   95.8%; Score 552; DB 1; Length 129;
  Best Local Similarity   95.5%; Pred. No. 1.4e-46;
  Matches 105; Conservative   1; Mismatches   4; Indels   0; Gaps   0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
             |||||||||||||||||||||||||||||:||||||||||||||||||||:||||| |||
Db   20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTGNYANWVQEKPDHLFTGLIGGTNNRAPGV 79

Qy   61 PARSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 PARSGSLIGDKAALTITGAQTEDEAIYPCALWYSNHWVFGGGTKLTVLG 129

RESULT 2
LV1E_MOUSE
ID   LV1E_MOUSE   STANDARD;   PRT;   129 AA.
AC   P01727;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda-1 chain V region S43 precursor.

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82220143; PubMed=6283385;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Somatic variants of murine immunoglobulin lambda light chains.";
RL   Nature 298:380-382(1982).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01724; 1A6V.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    129       Ig lambda-1 chain V region S43.
FT   DOMAIN       20    125       Ig-like.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  13529 MW;  84E54E7DD5791345 CRC64;

Query Match             95.8%;  Score 552;  DB 1;  Length 129;
Best Local Similarity   95.5%;  Pred. No. 1.4e-46;
Matches  105;  Conservative  1;  Mismatches  4;  Indels  0;  Gaps  0;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              |||||||||||||||||||||||||||||||||| |||||||||||||||||| ||| |||
Db         20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 79

Qy         61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
              |||||||||||||||||| ||||||| |||||||||||||||||||||||
Db         80 PARFSGSLIGDKAALTITGTQTEDEAMYFCALWYSNHWVFGGGTKLTVLG 129
```

RESULT 3

```
ID   LV1B_MOUSE     STANDARD;      PRT;   129 AA.
AC   P01724;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE OF 1-29 (MOPC 104E), AND REVISIONS TO 20 AND 26.
     MEDLINE=77148916; PubMed=403522;
RA   Burstein Y., Schechter I.;
RT   "Amino acid sequence of the NH2-terminal extra piece segments of the
RT   precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT   chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN   [2]
RP   SEQUENCE OF 20-129 (MOPC 104E AND RPC 20).
     MEDLINE=71107854; PubMed=5276767;
RA   Appella E.;
RT   "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
RN   [3]
RP   REVISIONS (MOPC 104E).
     MEDLINE=73229669; PubMed=4516208;
RA   Appella E.;
RT   Unpublished results, cited by:
RA   Cesari I.M., Weigert M.;
RL   Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
RN   [4]
RP   SEQUENCE OF 20-129 (J558 AND S104).
RX   MEDLINE=73229669; PubMed=4516208;
RA   Cesari I.M., Weigert M.;
RT   "Mouse lambda-chain sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
CC   -!- MISCELLANEOUS: Compositions and partial sequences of RPC 20 show
CC       no differences from MOPC 104E. The sequences of J558 and S104
CC       seems identical with that shown.
CC   -!- MISCELLANEOUS: These proteins were isolated from serum or urine of
CC       tumor-bearing mice.
CC   -!- MISCELLANEOUS: The MOPC 104E precursor was synthesized in a cell-
CC       free system directed by mRNA isolated from MOPC 104E myeloma
CC       polysomes. Met-1 was lacking in 90% of the chains. It is probably
CC       rapidly cleaved after synthesis.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; B93815; LIMS4E.
DR   PDB; 1A6U; X-ray; L=21-128.
DR   PDB; 1A6V; X-ray; L/M/N=20-129.
DR   PDB; 1A6W; X-ray; L=21-129.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    129       Ig lambda-1 chain V region MOPC
FT                               104E/RPC20/J558/S104.
FT   DOMAIN       20    125       Ig-like.
FT   MOD_RES      20     20       Pyrrolidone carboxylic acid.
FT   STRAND       23     25
FT   STRAND       28     31
FT   TURN         33     34
FT   STRAND       36     43
FT   TURN         44     45
FT   STRAND       46     46
FT   HELIX        50     52
FT   STRAND       55     60
FT   TURN         61     63
FT   STRAND       64     70
FT   TURN         71     73
FT   STRAND       74     75
FT   TURN         77     78
FT   STRAND       81     82
FT   STRAND       83     88
FT   TURN         89     90
FT   STRAND       91     97
FT   HELIX       101    103
FT   HELIX       105    112
FT   STRAND      117    119
FT   STRAND      123    127
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  13479 MW;  03629939D5791AC0 CRC64;

Query Match             95.7%;  Score 551;  DB 1;  Length 129;
Best Local Similarity   95.5%;  Pred. No. 1.80e-46;
Matches  105;  Conservative  2;  Mismatches  3;  Indels  0;  Gaps  0;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              ||||||||||||||||||||||||||||||||||:|||||||||||||||||: |||:|||
Db         20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 79

Qy         61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
              ||||||||||||||||||:||||||||:||||||||||||||||||||||
Db         80 PARFSGSLIGDKAALTITGTQTEDEAMYFCALWYSNHWVFGGGTKLTVLG 129
```

RESULT 4

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ID   Q8VDE2      PRELIMINARY;     PRT;   129 AA.
AC   Q8VDE2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
```

```
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin lambda chain variable region (Fragment).
GN   Name=4G12-A-H10;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Melle G.;
RL   Thesis (1995), Department of Ecole Superieure de Technicien en
RL   Biologie Biochimie, Universite Catholique de Lyon, Lyon, France.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Blachere T.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ291694; CAC82790.1; -.
DR   HSSP; P01724; 1A6V.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1     1
FT   NON_TER   129   129
SQ   SEQUENCE   129 AA; 13565 MW; C07F71003803ADBE CRC64;

Query Match   93.8%;   Score 540; DB 2; Length 129;
Best Local Similarity   93.6%;
Matches 103; Conservative  2; Mismatches  5; Indels  0; Gaps  0;

Qy   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDYLFTGLIGGTNNRPPGV  79

Qy  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  80  PARFSGSLIGDKAALTITGAQTEDEAMYFCVLWYSNHWVPGGGTKLTVLG  129
```

```
RESULT 5
ID   Q8CGS1                PRELIMINARY;   PRT;   113 AA.
AC   Q8CGS1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-deoxynivalenol scFv lambda light chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Wang Z., Munshi K., Osawa F., Pestka J.J., Hart L.P.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY151141; AAN75453.1; -.
DR   HSSP; P01724; 1A6V.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   113   113
SQ   SEQUENCE   113 AA; 12034 MW; 0C4A4C6597E22BE CRC64;

Query Match   93.0%;   Score 535.5; DB 2; Length 113;
Best Local Similarity   94.6%;   Pred. No. 5.3e-45;
Matches 105; Conservative  0; Mismatches  5; Indels  1; Gaps  1;

Qy   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
           |||||||||||||||||||||||||||||||||||||||| |||||||||||| || ||
Db   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTALGGGTNNRPPGV  60

Qy  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNH-WVFGGGTKLTVLG  110
           |||||||||||||||||||||||||||||||||||| |||||||||||||
Db  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHFWVFGGGTKLTVLG  111
```

```
RESULT 6
ID   LVIC_MOUSE             STANDARD;   PRT;   110 AA.
AC   P01725;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda-1 chain V region S178.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=73229669; PubMed=4516208;
RA   Cesari I.M., Weigert M.;
RT   "Mouse lambda-chain sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
CC   -!- MISCELLANEOUS: This protein was isolated from serum or urine of
CC       tumor-bearing mice.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01724; 1A6V.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN     1    106    Ig-like.
FT   NON_TER    1    1
FT   NON_TER  106    106
SQ   SEQUENCE   110 AA; 11654 MW; 7D06718E1A5302D6 CRC64;

Query Match   92.7%;   Score 534; DB 1; Length 110;
Best Local Similarity   92.7%;   Pred. No. 7.2e-45;
Matches 102; Conservative  3; Mismatches  5; Indels  0; Gaps  0;

Qy   1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
           ||||||||||||||||||||||||||||||||||||| |||||| :||||| ||  ||
Db   1  QAVVTQESALTTSPGETVTLTCRSNTGAVTTSNYANWVQQKPDYLFTGLIGNTNNRPPGV  60

Qy  61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  PARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNRWVFGGGTKLTVLG  110
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RESULT 7
ID   Q9ET13                PRELIMINARY;   PRT;   109 AA.
AC   Q9ET13;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Imunoglobulin light chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Song M.-Y., Kang H.-K., Kwag W.-J., Moon H.-J., Song T.-H., Ko I.-Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
```

RESULT 8
LV2B_MOUSE

ID LV2B_MOUSE STANDARD; PRT; 129 AA.
AC P01729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-2 chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274221; PubMed=6287422;
RA Wu G.E., Govindji N., Hozumi N., Murialdo H.;
RT "Nucleotide sequence of a chromosomal rearranged lambda 2
RT immunoglobulin gene of mouse.";
RL Nucleic Acids Res. 10:3831-3843(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82220143; PubMed=6283385;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains.";
RL Nature 298:380-382(1982).
RN [3]
RP SEQUENCE OF 1-22.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845(1979).
RN [4]
RP SEQUENCE OF 20-129.
RX MEDLINE=74048693; PubMed=4760498;
RA Dugan E.S., Bradshaw R.A., Simms E.S., Eisen H.N.;
RT "Amino acid sequence of the light chain of a mouse myeloma protein
RT (MOPC-315).";
RL Biochemistry 12:5400-5416(1973).
RN [5]
RP DETERMINATION OF AMIDATION STATES OF 58; 59; 62; 100; 102 AND 115.
RX MEDLINE=78187254; PubMed=418802;
RA Gavish M., Zakut R., Wilchek M., Givol D.;
RT "Preparation of a semisynthetic antibody.";
RL Biochemistry 17:1345-1351(1978).
CC -!- MISCELLANEOUS: This chain is from a myeloma protein with anti-DNP
CC   activity.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93431; L2MS35.
DR EMBL; AF287275; AAG03053.1; -.
DR HSSP; P01724; 1A6V.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11554 MW; 4F91BD351B1E158 CRC64;

Query Match 93.6%; Score 530.5; DB 2; Length 109;
Best Local Similarity 93.6%; Pred. No. 1.6e-44;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
         ||||||||||||||||:||||||||||| |||:|.|||||||||||||||||::|||||
Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAITTNNFANWVQEKPDHLFTGLIGDTNNRVPGV 60

Qy 61 PARFSGSLLIGDKAALTITGAQTEDDEAIYFCALWYSNHWVFGGGTKLTVIG 110
         ||||||| |||||||||||||||||:|||||||||:.-.|||||||||||||
Db 61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALMY-NNWVFGGGTKLTVIG 109

RESULT 9
LV1A_MOUSE

ID LV1A_MOUSE STANDARD; PRT; 117 AA.
AC P01723;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda-1 chain V region precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79084170; PubMed=103630;
RA Bernard O., Hozumi N., Tonegawa S.;
RT "Sequences of mouse immunoglobulin light chain genes before and after
RT somatic changes.";
RL Cell 15:1133-1144(1978).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR EMBL; V00811; CAA24193.1; -.
DR PIR; A01994; L1MSV.
DR HSSP; P01724; 1A6V.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 117 Ig lambda-1 chain V region.
FT DOMAIN 21 >117 Ig-like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12222 MW; 36F3C5601C54B55A CRC64;

Query Match 84.5%; Score 487; DB 1; Length 117;

(Additional DR/feature block, lambda-2 chain V region MOPC 315:)

DR HSSP; P01724; 1A6V.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 19
FT CHAIN 20 129 Ig lambda-2 chain V region MOPC 315.
FT DOMAIN 20 125 Ig-like.
FT MOD_RES 20 20 Pyrrolidone carboxylic acid.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13418 MW; 0AA6E812S723552C CRC64;

Query Match 89.2%; Score 514; DB 1; Length 129;
Best Local Similarity 88.2%; Pred. No. 8e-43;
Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
         |||||||||||||||.|||||||||||||||||.|||.|||||||||||||||| .| ||
Db 20 QAVVTQESALTTSPGGTVTLTCRSSTGAVTTSNYANWIQEKPDHLFTGLIGGTSNRAPGV 79

Qy 61 PARFSGSLLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
         | ||||||.|||||||||||||||||:|.|||||:.:|:.|||||||.||||
Db 80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWFRNHFVFGGGTKVTVLG 129

Best Local Similarity   96.9%; Conservative 0; Pred. No. 3.3e-40;
Matches 94;   Mismatches 3; Indels   0; Gaps   0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRVPGV 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRVPGV 80

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNH 97
            |||||||||||||||||||||||||||||||||||||
Db   81 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNH 117

RESULT 10
ID   LV2A_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01728;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda-2 chain V region precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=78179064; PubMed=418414;
RA   Tonegawa S., Maxam A.M., Tizard R., Bernard O., Gilbert W.;
RT   "Sequence of a mouse germ-line gene for a variable region of an
RT   immunoglobulin light chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 75:1485-1489(1978).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; J00599; AAA39167.1; -.
DR   EMBL; V00815; CAA24196.2; -.
DR   EMBL; X58412; CAA41313.1; -.
DR   EMBL; X58418; CAA41318.1; -.
DR   EMBL; X58423; CAA41323.1; -.
DR   EMBL; X58424; CAA41324.1; -.
DR   PIR; A01996; L2MSWE.
DR   HSSP; P01724; 1A6V.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   19
FT   CHAIN   20   117   Ig lambda-2 chain V region.
FT   DOMAIN   20   >117
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 12222 MW; 43FDR19T419B42A6 CRC64;

Query Match   79.9%; Score 460; DB 1; Length 117;
Best Local Similarity   89.8%; Pred. No. 1.5e-37;
Matches 88; Conservative 3; Mismatches 7; Indels   0; Gaps   0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANMVQEKPDHLFTGLIGGTINRVPGV 60
            |||||||||||||||||||||||||||||||: ||||||||||||||||||||||||||||
Db   20 QAVVTQESALTTSPGGTVILTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTTSNRAPGV 79

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHW 98
            |||||||||||||||||||||||||||||||||||||:
Db   80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHF 117

RESULT 11
ID   LV0A_HUMAN   STANDARD;   PRT;   117 AA.
AC   P04211;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V region 4A precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014122; PubMed=6091030;
RA   Anderson M.L.M., Szajnert M.F., Kaplan J.C., McColl L., Young B.D.;
RT   "The isolation of a human Ig V lambda gene from a recombinant library
RT   of chromosome 22 and estimation of its copy number.";
RL   Nucleic Acids Res. 12:6647-6661(1984).
DR   PIR; A01993; LVHU2.
DR   HSSP; P01724; 1A6V.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   117   Ig lambda chain V region 4A.
FT   DOMAIN   21   117   Framework-1.
FT   DOMAIN   42   55   Complementarity-determining-1.
FT   DOMAIN   56   71   Framework-2.
FT   DOMAIN   72   78   Complementarity-determining-2.
FT   DOMAIN   79   110   Framework-3.
FT   DOMAIN   111   117   Complementarity-determining-3.
FT   DISULFID   42   110   By similarity.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 12380 MW; C587B0047CC1CD62 CRC64;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGYYPNWFQQKPGQAPRALIYSTSNKHSWT 80

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWY 94
            |||||||||||||||:||||: |:
Db   81 PARFSGSLIGGKAALTLSGVQPEDEABYYCLLYY 114

RESULT 12
ID   LV6C_HUMAN   STANDARD;   PRT;   111 AA.
AC   P06317;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig lambda chain V-VI region SUT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Solomon A., Kyle R.A., Frangione B.;
RT   "Light chain variable region subgroups of monoclonal immunoglobulins
RT   in amyloidosis AL.";

RL   (In) Glenner G.G., Osserman E.F., Benditt E.P., Calkins E.,
RL   Cohen A.S., Zucker-Franklin D. (eds.);
RL   Amyloidosis, pp.449-462, Plenum Press, New York (1986).
DR   PIR; A01988; L6HUST.
DR   PDB; 1CD0; X-ray; A/B=1-111.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN   1   22   Framework-1.
FT   DOMAIN   23   35   Complementarity-determining-1.
FT   DOMAIN   36   50   Framework-2.
FT   DOMAIN   51   57   Complementarity-determining-2.
FT   DOMAIN   58   91   Framework-3.
FT   DOMAIN   92   100   Complementarity-determining-3.
FT   DOMAIN   101   111   Framework-4.
FT   DISULFID   22   91   By similarity.
FT   STRAND   4   5
FT   STRAND   9   12
FT   TURN   14   15
FT   STRAND   18   24
FT   HELIX   29   31
FT   STRAND   35   39
FT   TURN   41   42
FT   TURN   46   50
FT   STRAND   51   53
FT   STRAND   54   54
FT   TURN   57   58
FT   STRAND   61   62
FT   STRAND   63   68
FT   STRAND   69   72
FT   STRAND   73   78
FT   HELIX   83   85
FT   STRAND   87   95
FT   TURN   96   97
FT   STRAND   98   102
FT   STRAND   105   109
FT   NON_TER   111   111
FT   NON_TER   111   111
SQ   SEQUENCE   111 AA; 12247 MW; 0941DD547D983598 CRC64;

RESULT 13
Q9NSD6
ID   Q9NSD6   PRELIMINARY;   PRT;   107 AA.
AC   Q9NSD6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Homo sapiens This CDS feature is included to show the translation of
DE   the corresponding V region. Presently translation qualifiers on
DE   V region features are illegal. (Fragment)
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocyte;
RA   Hohmann A.;

Query Match   42.4%; Score 244.5; DB 1; Length 111;
Best Local Similarity   46.4%; Pred. No. 2.6e-16;
Matches   51; Conservative   19; Mismatches   37; Indels   3; Gaps   2;

Qy   3 VVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVPA   62
            |||:| | ||| ||:: :: :|||:||: |:||| | :|| || |::|||:|::|||
Db   3 MLTQPHSVSESPGKTVIISCTRSDGTI-AGYYVQWYQQRPGRAPTIVIFEDTQRPSGVPD   61

Qy   63 RFSGSL--IGDKAALTITGAQTEDEAIYFCALWYSNHHWVFGGGTKLTVLG   110
            |||||: |||| |||: :||::||:|| |:|: :::||||||||||||
Db   62 RFSGSIDRSSNSASLTISGLQTEDEADYYCQSYDRDHWVFGGGTKLTVLG   111

RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L43092; AAA69746.2; -.
DR   PIR; S70444; S70444.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   107   107
FT   NON_TER   1   1
SQ   SEQUENCE   107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match   41.6%; Score 239.5; DB 2; Length 107;
Best Local Similarity   50.5%; Pred. No. 7.7e-16;
Matches   55; Conservative   15; Mismatches   34; Indels   5; Gaps   2;

Qy   4 VTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVPAR   63
            :|||:| || ::| :||:||: |: |:| ||:| |:|| || |::|:||::||||::
Db   2 LTQDPVVSVALGQTVRITCQ---GDSLRSYYASWIQQKPGQAPVLVIYGKNNRPSGIPDR   58

Qy   64 FSGSLIGDKAALTITGAQTEDEAIYFCALWYS--NHWVFGGGTKLTVLG   110
            ||||: |||| |||:|||::||:| |::|: |||||||||||||||
Db   59 FSGSSGNTASLTITGAQAEDEADYYCNSRDSSGNHAVFGGGTKLTVLG   107

RESULT 14
Q6GMV7
ID   Q6GMV7   PRELIMINARY;   PRT;   236 AA.
AC   Q6GMV7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073795; AAH73795.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.

```
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;   24950 MW;   3B047724784 7B930 CRC64;

Query Match             41.5%;  Score 239;  DB 2;  Length 236;
Best Local Similarity   46.0%;  Pred. No. 2.1e-15;
Matches   52;  Conservative   20;  Mismatches   37;  Indels   4;  Gaps   2;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              | ::|  ||||  :| |  :|| :|||: || ::|| | | :|||  ||  |||||
Db         20 QSVLTQPSSVSGTPGQRVTISCSGSSSNI-GANNVNWYQQLPGTAPKLLIHTNQRPSGV 78

Qy         61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALW---YSNHWVFGGGTKLTVLG 110
              |  ||||   |  |   |  |  :|| || ||      ||  ||||||||||||
Db         79 PERFSGSKSGPSASLVISGLQSEDEAEYYCAAWDDSLDGPYVFGTGTKVTVLG 131
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RESULT 15
```
ID   LV2C_HUMAN             STANDARD;     PRT;   111 AA.
AC   P01706;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-II region BOH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75115478; PubMed=804002;
RA   Kohler H., Rudofsky S., Kluskens L.;
RT   "The primary structure of a human lambda II chain.";
RL   J. Immunol. 114:415-421(1975).
CC   -!- MISCELLANEOUS: The C region of this chain has the OZ+ marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A01972; L2HUBH.
HSSP; P01709; 2MCG.
DR   SMART; SM00406; IGv; 1.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrrolidone carboxylic acid.
DOMAIN          1    106       Ig-like.
MOD_RES         1      1       Pyrrolidone carboxylic acid.
DISULFID       22     90       By similarity.
NON_TER       111    111
SQ   SEQUENCE   111 AA;   11650 MW;   94520993262388 CRC64;

Query Match             41.1%;  Score 236.5;  DB 1;  Length 111;
Best Local Similarity   44.1%;  Pred. No. 1.6e-15;
Matches   49;  Conservative   21;  Mismatches   40;  Indels   1;  Gaps   1;

Qy          1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
              || :|| || |  :|  ||  :| :|: || ::||  || | :|||  ||  |||||
Db          1 QSALTQPRSVSGSPGQSVTISCAGTSSDVGGNHFVSWYQQHPGKAPKLIIYGVNKRPSGV 60

Qy         61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYSNH-WVFGGGTKLTVLG 110
              | ||||| || | ||| ||||:||||| || | :|  ||||||||| ||||
Db         61 PYRFSGSKSGNTASLTISGLQAEDEAHYCCSYAGRFTWVFGGGTNLTVLG 111
```

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 17:46:45 ; Search time 15.0885 Seconds
(without alignments)
701.451 Million cell updates/sec

Title: US-10-774-076-5
Perfect score: 576
Sequence: 1 QAVVTQESALTTSPGETVTL.........ALWYSNHWVFGGGTKLTVLG 110
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	553	96.0	128	2	S52450	Ig lambda chain v
2	553	96.0	287	4	PC4402	pelB leader/Ig hea
3	551	95.7	129	1	L1MS4B	Ig lambda-1 chain
4	546	94.8	214	2	PC4156	Ig lambda chain v
5	535.5	93.0	112	2	S06818	Ig lambda chain v
6	532	92.4	113	2	S06819	Ig lambda chain v
7	522	90.6	106	2	S20654	Ig lambda chain v
8	522	90.6	113	2	B54256	Ig lambda-1 chain
9	520.5	90.4	114	2	S06820	Ig lambda chain v
10	514	89.2	129	2	L2MS35	Ig lambda-2 chain
11	512	88.8	113	2	S06821	Ig lambda chain v
12	511.5	88.8	114	2	S06822	Ig lambda chain v
13	498	86.5	99	2	S14582	Ig lambda chain v
14	489.5	85.0	99	2	S14582	Ig lambda chain v
15	487	85.0	97	2	PH1090	Ig lambda chain v
16	487	84.5	116	2	L1MSV	Ig lambda-1 chain
17	486	84.4	100	2	PH1088	Ig lambda chain v
18	481	83.5	99	2	S14584	Ig lambda chain v
19	471	81.8	100	2	PH1087	Ig lambda chain v
20	468	81.2	99	2	S14586	Ig lambda chain v
21	467	81.1	99	2	S14586	Ig lambda chain v
22	460	79.9	117	2	L2MSWB	Ig lambda chain v
23	457	79.3	99	2	S14585	Ig lambda chain v
24	448	77.8	92	2	A27633	Ig lambda-2 chain
25	416	72.2	116	2	C27390	Ig lambda chain pr
26	317.5	55.1	120	2	S30528	Ig lambda chain v
27	308.5	53.6	136	2	S4610	ARMlambda protein
28	289.5	50.3	235	2	S25749	Ig lambda chain -
29	282	49.0	112	2	S26655	Ig lambda chain v
30	280.5	48.7	110	1	2	S57465	Ig lambda chain V-
31	279	48.4	117	1	2	LVHU2	Ig lambda chain pr
32	279	48.4	117	1	2	S04526	Ig lambda chain pr
33	277	48.1	98		2	S36062	Ig lambda chain -
34	277	43.4	250		2	S36063	Ig lambda chain -
35	247.5	43.0	108		2	S38498	Ig lambda chain -
36	246.5	42.8	110	1	2	S57442	Ig lambda chain V-
37	244.5	42.4	111	1	2	L6HUST	Ig lambda chain (B
38	244.5	42.4	216		2	A42193	Ig lambda chain V-
39	243.5	42.3	109		2	S19663	Ig lambda chain V-
40	241	41.8	149		2	S23626	Ig lambda chain V
41	241	41.8	213		2	S21066	Ig lambda chain V
42	240	41.7	217		2	JE0246	Ig lambda chain V
43	239.5	41.6	233		2	S25744	Ig lambda chain NI
44	238.5	41.4	233		2	S25752	Ig lambda chain -
45	237.5	41.2	108		2	S47184	Ig lambda chain -

ALIGNMENTS

RESULT 1
S52450
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52450
R;Berdoz, J.; Kraehenbuhl, J.P.
A;Reference number: S52450
A;Description: Specific amplification by the polymerase chain reaction of rearranged ge
submitted to the EMBL Data Library, November 1994
A;Cross-references: EMBL:X82687; NID:g673448; PIDN:CAA58008.1; PID:g673449
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
A;Residues: 1-128 <BER>
A;Status: preliminary
A;Molecule type: DNA
F;34-111/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 553; DB 2; Length 128;
Best Local Similarity 97.2%; Pred. No. 1.5e-41;
Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy  1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
       ||||||||||||||||||||||||||||||||| |||| ||||||||||||||| ||||| |||
Db  20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQBKPDHLFTGLIGGTNNRAPGV  79

Qy  61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL  109
       ||||||||||||||||||||||||||||||||||||||||||||||||
Db  80 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL  128
```

RESULT 2
PC4402
pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein
C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C;Accession: PC4402
R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997
A;Title: Construction, bacterial expression, and characterization of hapten-specific si
A;Reference number: PC4402
A;Accession: PC4402
A;Molecule type: DNA
A;Residues: 1-287 <SUZ>
C;Keywords: fusion protein

Query Match 96.0%; Score 553; DB 4; Length 287;
Best Local Similarity 97.2%; Pred. No. 3.4e-41;
Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     26 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 85

Qy     61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     86 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 134
```

RESULT 3
L1MS4E
Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43) -
d after synthesis
C;Species: Mus musculus (house mouse)
C;Date: 24-Sep-1981 #sequence revision 24-Sep-1981 #text_change 09-Jul-2004
A;Accession: B93815; B93775; C93775; A93784; B93784; C93784; A90780; C93282; A01995
R;Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104E
A;Accession: B93815
A;Molecule type: protein
A;Residues: 1-29 <BUR>
A;Cross-references: UNIPROT:P01724
A;Note: this precursor was synthesized in a cell-free system directed by messenger RNA i

R;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; MUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
A;Molecule type: protein
A;Accession: C93775
A;Residues: 'Z',21-25,'Q',27-129 <APP>

R;Cesari, I.M.; Weigert, M.
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
A;Reference number: A93784; MUID:73229669; PMID:4516208
A;Contents: J558; S104; S178
A;Molecule type: protein
A;Accession: A93784
A;Residues: 20-129 <AP2>
A;Accession: B93784
A;Residues: 20-129 <CBS>
A;Accession: C93784
A;Residues: 20-129 <CE2>
A;Residues: 20-43,'N',45-70,'N',72-115,'R',117-129 <CE3>

R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch
A;Reference number: A90780; MUID:79084170; PMID:103630
A;Molecule type: protein
A;Accession: A90780
A;Residues: 20-129 <CES>

R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Contents: S43
A;Molecule type: DNA
A;Accession: C93282
A;Residues: 1-58,'E',60-89,'D',91-98,'T',100-105,'M',107-129 <BOT>
A;Residues: 1-43,'T',45-50,'G',52-58,'E',60-89,'D',91-129 <BER>
A;Note: the sequence was determined from the differentiated gene
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.

C;Genetics:
A;Introns: 16/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k-
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C;Keywords: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; Pyroglutamic acid
F;1-19/Domain: signal sequence #status experimental <SIG>
F;20-129/Domain: Ig lambda chain precursor V region #status experimental <MAT>
F;34-111/Domain: immunoglobulin homology <IMM>
F;20/Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F;41-109/Disulfide bonds: #status predicted

Query Match   95.7%; Score 551; DB 1; Length 129;
Best Local Similarity   95.5%; Pred. No. 2.3e-41;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||||||   ||||||||||||||||| |||||
Db     20 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYASWVQEKPDHLFTGLIGGTNNRAPGV 79

Qy     61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||| |||||||||||||||||||||||||||||||||||||||
Db     80 PARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 129
```

RESULT 4
PC4156
Ig lambda chain V region MabB23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4156
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A;Reference number: PC4155; MUID:96194809; PMID:8647454
A;Accession: PC4156
A;Molecule type: mRNA
A;Residues: 1-214 <KWA>
A;Cross-references: GB:U28967; NID:g1262178; PIDN:AAC52488.1; PID:g1262179
A;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-214/Product: light chain #status predicted <MAT>
F;98-110/Region: V region
F;130-198/Domain: immunoglobulin homology <IMM>

Query Match   94.8%; Score 546; DB 2; Length 214;
Best Local Similarity   95.5%; Pred. No. 1e-40;
Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||||||   ||||||||||||||||| |||||
Db      1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYASWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy     61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||| |||||||||||||||||||||||||||||||||||||||
Db     61 PARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
```

RESULT 5
S06818
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06818
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06818
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-112 <MIL>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

```
Qy      1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||||||   ||||||||||||||||| |||||
Db      1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYASWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy     61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||| |||||||||||||||||||||||||||||||||||||||
Db     61 PARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
```

F;15-92/Domain: immunoglobulin homology <IMM>

```
Query Match              93.0%;   Score 535.5;  DB 2;  Length 112;
Best Local Similarity    94.5%;   Pred. No. 4.4e-40;
Matches 104;  Conservative 2;  Mismatches 3;  Indels 1;  Gaps 1;

Qy    2 AVVTQESA-LTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||||||||||||||||||||||||||||||||||||| |||
Db   61 PARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
```

RESULT 6
S06819
Ig lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: S06819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06819
A;Molecule type: mRNA
A;Residues: 1-113 <MIL>
A;Cross-references: EMBL:X17168; NID:g52251; PIDN:CAA35046.1; PID:g930172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology <IMM>
F;21-89/Disulfide bonds: #status predicted

```
Query Match              92.4%;   Score 532;  DB 2;  Length 113;
Best Local Similarity    95.4%;   Pred. No. 9.1e-40;
Matches 103;  Conservative 1;  Mismatches 4;  Indels 0;  Gaps 0;

Qy    2 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVP 61
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 60

Qy   62 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ARFSGSLIGDKAALTITGAQTEDEAIYFCSLWYSNHLVFGGGTKLTVL 108
```

RESULT 7
S20654
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S20654
R;Losman, M.; Fagy, T.M.; Novick, K.B.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20654
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-106 <LOS>
A;Cross-references: EMBL:X65012; NID:g52705; PIDN:CAA46145.1; PID:g52706
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin <IMM>
F;15-92/Domain: immunoglobulin homology <IMM>

```
Query Match              90.6%;   Score 522;  DB 2;  Length 106;
Best Local Similarity    94.3%;   Pred. No. 6.4e-39;
Matches 100;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;

Qy    1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 QAVVTQESALITSPGETVTLTCRSSIGAVTTSNYAYWVQKPDHLFTGLIGGTNNRAPGV 60
```

Qy
Db

```
Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKL 106
         |||||||||||||||||||||||||||||||||||||||||||||
Db   61 PVRFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKL 106
```

RESULT 8
B54256
Ig lambda-1 chain V region (hybridoma Se155-4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B54256; A44592
A;Molecule type: protein
A;Residues: 1-113 <BUN>
A;Experimental source: Se155-4 hybridoma, BALB/c mouse
A;Note: sequence extracted from NCBI backbone (NCBIP:146746)
A;Note: the Se155-4 hybridoma is specific for the 3,6-dideoxy-D-galactose epitope of th
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
R;Bundle, D.R.; Eichler, E.; Gidney, M.A.; Meldal, M.; Ragauskas, A.; Sigurskjold, B.W.
Biochemistry 33, 5172-5182, 1994
A;Title: Molecular recognition of a Salmonella trisaccharide epitope by monoclonal anti
A;Reference number: A54256; MUID:94227048; PMID:7513555
A;Accession: B54256

```
Query Match              90.6%;   Score 522;  DB 2;  Length 113;
Best Local Similarity    90.0%;   Pred. No. 6.8e-39;
Matches 99;  Conservative 3;  Mismatches 8;  Indels 0;  Gaps 0;

Qy    1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
         |||||||||||||||||||||||||||||||| ||||  || |||||||||||||  |||
Db    1 QAVVTQESALTTSPGETVTLTCRSSTGVTSGNHANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
         |||||||||||||||||||||| ||||||||||||||||||||||||||
Db   61 PARFSGSLIGDKAALTITGAQPEDEAIYFCALWCNNHWIFGGGTKLTVLG 110
```

RESULT 9
S06820
Ig lambda chain V region (clone 12D4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06820
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06820
A;Molecule type: mRNA
A;Residues: 1-114 <MIL>
A;Cross-references: EMBL:X17169
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin <IMM>
F;22-90/Disulfide bonds: #status predicted

```
Query Match              90.4%;   Score 520.5;  DB 2;  Length 114;
Best Local Similarity    94.5%;   Pred. No. 9.2e-39;
Matches 103;  Conservative 0;  Mismatches 5;  Indels 1;  Gaps 1;

Qy    2 AVVTQES-ALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
         ||||||| |||||||||||||||||||||||||||| |||||||||||||||   |||||
Db    1 AVVTQESIXLTTSPGETVTLTCRSSTGVTSGNHANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHLVFGGGTKLTVL 109
```

Qy
Db

RESULT 10
L2MS35

Ig lambda-2 chain precursor V region (MOPC 315) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
R;Wu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.
Nucleic Acids Res. 10, 3831-3843, 1982
A;Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene of
A;Reference number: A93431; MUID:82274221; PMID:6287422
A;Accession: A93431
A;Molecule type: mRNA
A;Residues: 1-129 <WUG>
A;Cross-references: UNIPROT:P01729
R;Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Nature 298, 380-382, 1982
A;Reference number: A91462; MUID:79148758; PMID:428562
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
Fed. Proc. 38, 1839-1845, 1979
A;Title: Structure and function of immunoglobulin genes and precursors.
A;Accession: B93282; MUID:82220143; PMID:6283385
A;Molecule type: DNA
A;Note: the sequence was determined from the differentiated gene
A;Accession: A90372
A;Reference number: A90372; MUID:74048693; PMID:4760498
A;Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).
Biochemistry 12, 5400-5416, 1973
R;Dugan, E.S.; Bradshaw, R.A.; Simms, E.S.; Eisen, H.N.
A;Residues: 1-22 <SCH>
A;Molecule type: protein
A;Reference number: A90410; MUID:78187254; PMID:418802
A;Accession: A90410
A;Title: Preparation of a semisynthetic antibody.
Biochemistry 17, 1345-1351, 1978
R;Gavish, M.; Zakut, R.; Wilchek, M.; Givol, D.
A;Residues: 20-24,'E',26-73,'D',75-129 <DUG>
A;Molecule type: protein
A;Accession: S09372
A;Reference number: S09391; MUID:90005397; PMID:2792076
A;Title: Minimum length of an idiotypic peptide and a model for its binding to a major h
EMBO J. 8, 1947-1952, 1989
R;Bogen, B.; Lambris, J.D.
A;Residues: 110-126 <BOG>
A;Molecule type: protein
A;Accession: S09391
A;Comment: This chain is from a myeloma protein with anti-DNP activity.
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; pyroglutamic acid
F;1-19/Domain: signal sequence #status experimental <SIG>
F;20-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>
F;34-111/Domain: immunoglobulin homology <IMM>
F;110-126/Region: idiotype to histocompatibility complex class II #status experimental
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;41-109/Disulfide bonds: #status predicted

Query Match
Best Local Similarity   89.2%;   Score 514;   DB 1;   Length 129;
Matches   97; Conservative   6; Mismatches   7; Indels   0; Gaps   0;

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Qy    1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV  60
Db   20  QAVVTQESALTTSPGTVILTCRSSTGAVTTSNYANWIQEKPDHLFTGLIGGTINRVPGV  79

Qy   61  PARFSGSLIGDKAALTITGAQTEDDAIYFCALWYSNHWVFGGGTKLTVLG  110
Db   80  PVRFSGSLIGDXAALTITGAQTEDDAMYFCALWFRNHFVPGGGTKVTVLG  129
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RESULT 11
S06821
Ig lambda chain V region (clone 11C7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
A;Accession: S06821
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06821
A;Molecule type: mRNA
A;Residues: 1-113 <MIL>
A;Cross-references: EMBL:X17170; NID:g52253; PIDN:CAA35048.1; PID:g931174
A;Note: the authors translated the codon AGT for residue 47 as Gly, GTT for residue 56
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology <IMM>
F;21-89/Disulfide bonds: #status predicted

Query Match
Best Local Similarity   88.9%;   Score 512; DB 2; Length 113;
Matches   99; Conservative   1; Mismatches   9; Indels   0; Gaps   0;

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Db    1  AVVTQESILTTSPGETVTLTCRSSTGAVTTSNYANWIQEKPDHLFTSLIGGISNRVPGVP  60

Qy   62  ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
Db   61  ARFSGSLIGDKVALTIIGTQTEDEAIYFCALWYSNHLVFGGGTKLTVLG  109
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RESULT 12
S06822
Ig lambda chain V region (clone 3B9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
A;Accession: S06822
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06822
A;Molecule type: mRNA
A;Residues: 1-114 <MIL>
A;Status: not compared with conceptual translation
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match
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Db    1  AVVTQESAXLTTSPGETVTLTCRSSTGAVTTSNYANWIQEKPDHLFTSLIGGTNNRAPGV  60

Qy   61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
Db   61  PARFSGSLIGXKAALTITGAQTEDBDIYFCSLWYSNHLVFGGGTKLTVLG  110
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RESULT 13
S14582
Ig lambda chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
A;Accession: S14582; S14587; S14588
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Reference number: S14582; S14587; S14588
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH

A;Reference number: S14484
A;Accession: S14582
A;Molecule type: mRNA
A;Residues: 1-99 <CH3>
A;Cross-references: EMBL:X58654; NID:g52911; PIDN:CAA41511.1; PID:952912
A;Experimental source: isolate PPC-1-54
A;Accession: S14587
A;Molecule type: mRNA
A;Residues: 1-99 <CH2>
A;Cross-references: EMBL:X58659; NID:g52921; PIDN:CAA41516.1; PID:952922
A;Experimental source: isolate PPC-1-5
A;Accession: S14588
A;Molecule type: mRNA
A;Residues: 1-99 <CH3>
A;Cross-references: EMBL:X58660; NID:g52923; PIDN:CAA41517.1; PID:952924
A;Experimental source: isolate PPC-15-30
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWV 99
        |||||||||||||||||||||||||||||||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWV 99

RESULT 14
PH1089
Ig lambda chain V region (clone 165.33) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1089
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1089
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-99 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-92/Domain: immunoglobulin homology <IMM>

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Matches   95; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

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Db   1 QXVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWV 99
        ||||||||||||||||||||||||||||||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSN-WVF 99

RESULT 15
PH1090
Ig lambda chain V region (clone V-lambda-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1090
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1090
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
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Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNH 97
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Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNH 97

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Search completed: December 29, 2004, 18:06:57
Job time : 16.2552 secs

Query Match   85.0%; Score 489.5; DB 2; Length 99;
Best Local Similarity   96.0%; Pred. No. 4.1e-36;
Matches   96; Conservative   0; Mismatches   3; Indels   1; Gaps   1;

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Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVF 100
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OM protein - protein search, using sw model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on: December 29, 2004, 18:05:34 ; Search time 63.5988 seconds
                                                  (without alignments)
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Title: US-10-774-076-5
Perfect Score: 576
Sequence: 1 QAVVTQESALTTSPGETVTL..........ALWYSNHWVFGGGTKLTVLG 110

Scoring table: BLOSUM62
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Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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SUMMARIES

Result No.	Score	Query Match Length	% DB	DB ID	Description
1	576	100.0	17	17	US-10-774-076-5	Sequence 5, Appli
2	559	97.0	112	17	US-10-768-193-8	Sequence 8, Appli
3	555	96.4	110	17	US-10-379-392-159	Sequence 159, App
4	540	93.8	110	17	US-10-625-047-1	Sequence 1, Appli
5	535	92.9	109	17	US-10-625-047-21	Sequence 21, Appli
6	535	92.9	109	17	US-10-625-047-29	Sequence 29, Appli
7	532	92.4	109	17	US-10-625-047-22	Sequence 22, Appl
8	532	92.4	218	17	US-10-625-047-27	Sequence 27, Appl
9	531	92.2	109	17	US-10-625-047-23	Sequence 23, Appl
10	531	92.2	218	17	US-10-625-047-28	Sequence 28, Appl
11	530.5	92.1	9	17	US-09-865-483-7	Sequence 7, Appli
12	530.5	92.1	109	17	US-10-726-555-7	Sequence 7, Appli
13	530	92.0	108	14	US-10-305-268-4	Sequence 4, Appli
14	522	90.6	14	14	US-10-328-190-14	Sequence 14, Appl
15	519	90.1	16	16	US-10-768-193-8	Sequence 8, Appl
16	519	90.1	218	16	US-10-379-392-159	Sequence 159, App
17	517	89.8	16	16	US-09-940-727B-1	Sequence 1, Appl
18	513	89.1	109	10	US-09-940-727B-2	Sequence 2, Appl
19	508	88.2	107	14	US-10-328-190-10	Sequence 10, Appl
20	504	87.5	109	10	US-09-940-727B-3	Sequence 3, Appli
21	504	87.5	109	10	US-09-940-727B-121	Sequence 121, App
22	494	85.8	218	16	US-10-379-392-164	Sequence 164, App
23	493	85.6	218	16	US-10-379-392-161	Sequence 161, App
24	473	82.1	99	10	US-09-940-727B-92	Sequence 92, Appl
25	469	81.4	99	10	US-09-940-727B-88	Sequence 88, Appl
26	428	74.3	100	16	US-09-940-727B-96	Sequence 96, Appl
27	421	73.1	112	16	US-09-327-598-809	Sequence 809, App
28	413.5	71.8	98	10	US-09-940-727B-4	Sequence 4, Appli
29	391.5	68.0	252	9	US-09-750-424-1	Sequence 1, Appli
30	391.5	68.0	252	14	US-10-169-179-1	Sequence 1, Appli
31	338	58.7	245	10	US-09-880-748-1523	Sequence 1523, Ap
32	338	58.7	245	10	US-09-848-798-1523	Sequence 1523, Ap
33	329	57.1	108	10	US-09-848-798-52	Sequence 52, Appl
34	329	57.1	108	10	US-09-848-798-166	Sequence 166, App
35	329	57.1	108	10	US-09-848-798-53	Sequence 53, Appl
36	315.5	54.8	253	14	US-10-322-673-54	Sequence 54, Appl
37	315	54.7	108	10	US-09-848-798-53	Sequence 53, Appl
38	309	53.6	216	9	US-09-291-299A-8	Sequence 8, Appl
39	303.5	52.7	249	10	US-09-880-748-1838	Sequence 1838, Ap
40	303.5	52.7	249	14	US-10-293-418-1838	Sequence 1838, Ap
41	300	52.1	84	9	US-09-135-238B-5	Sequence 5, Appli
42	294.5	51.1	244	14	US-10-120-414-77	Sequence 77, Appl
43	292.5	50.8	251	10	US-09-880-748-890	Sequence 890, Appl
44	292.5	50.8	251	10	US-09-880-748-891	Sequence 891, App
45	292.5	50.8	251	10	US-09-880-748-894	Sequence 894, App

ALIGNMENTS

RESULT 1
US-10-774-076-5

; Sequence 5, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 110
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-5

Query Match   100.0%; Score 576; DB 17; Length 110;
Best Local Similarity 100.0%; Pred. No. 4e-46;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSAANWVQEKPDHLFTGLIGGTINRVPGV 60
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Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSAANWVQEKPDHLFTGLIGGTINRVPGV 60

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
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Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110

RESULT 2
US-10-816-938-8
; Sequence 8, Application US/10816938

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861.1670002
; CURRENT APPLICATION NUMBER: US/10/816,938
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 8
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-816-938-8

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Best Local Similarity   97.3%;          Score 559;  DB 17;   Length 112;
Matches  107;  Conservative   0;  Pred. No. 1.6e-44;  Mismatches   3;  Indels   0;  Gaps   0;

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         |||||||||||||||||||||||||||||||| ||||||||||||||||||| || |||
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Qy   61  PARFSGSSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
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RESULT 3
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US-10-816-938-21
; Sequence 21, Application US/10816938
; Publication No. US20040229301A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Baiyang
; TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
; FILE REFERENCE: 1861.1670002
; CURRENT APPLICATION NUMBER: US/10/816,938
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 21
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-816-938-21

Query Match             96.4%;
Best Local Similarity   96.4%;          Score 555;  DB 17;   Length 110;
Matches  106;  Conservative   1;  Pred. No. 3.6e-44;  Mismatches   3;  Indels   0;  Gaps   0;

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         |||||||||||||||||||||||||||||||| ||||||||||||||||||| || |||
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RESULT 4
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; Sequence 1, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: murine monoclonal antibody 2D12.5 light chain
; OTHER INFORMATION: variable domain (VL)
US-10-625-047-1

Query Match             93.8%;
Best Local Similarity   93.8%;          Score 540;  DB 17;   Length 110;
Matches  103;  Conservative   1;  Pred. No. 9e-43;  Mismatches   6;  Indels   0;  Gaps   0;

Qy    1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV   60
         |||||||||||||||||||||||||||||||| ||||||||||||||||||| || |||
Db    1  QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRPPGV   60

Qy   61  PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
         ||||||||||||||||| | ||||||||||||||||||||||||||:||||
Db   61  PARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTRLTVLG  110
```

RESULT 5
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US-10-625-047-21
; Sequence 21, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 21
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: native hybridoma murine 2D12.5 light chain
US-10-625-047-21

Query Match             92.9%;
Best Local Similarity   93.6%;          Score 535;  DB 17;   Length 109;
Matches  102;  Conservative   1;  Pred. No. 2.6e-42;  Mismatches   6;  Indels   0;  Gaps   0;

Qy    2  AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVP   61
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||| || |||
Db    1  AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRPPGVP   60

Qy   62  ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG  110
         |||||||||||||||| | ||||||||||||||||||||||||:||||
Db   61  ARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTRLTVLG  109
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RESULT 6
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US-10-625-047-29
; Sequence 29, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
```

```
;     CURRENT FILING DATE: 2003-07-22
;     PRIOR APPLICATION NUMBER: US 10/350,555
;     PRIOR FILING DATE: 2003-01-23
;     NUMBER OF SEQ ID NOS: 72
;     SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 29
;     LENGTH: 109
;     TYPE: PRT
;     ORGANISM: Mus musculus
;     FEATURE:
;     OTHER INFORMATION: native hybridoma murine 2D12.5 light chain
; US-10-625-047-29
;     OTHER INFORMATION: variable region (VL)

RESULT 7
US-10-625-047-22
; Sequence 22, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
;     APPLICANT: Meares, Claude
;     APPLICANT: Corneillie, Todd
;     APPLICANT: The Regents of the University of California
;     TITLE OF INVENTION: Multi-Functional Antibodies
;     FILE REFERENCE: 023070-13091OUS
;     CURRENT APPLICATION NUMBER: US/10/625,047
;     CURRENT FILING DATE: 2003-07-22
;     PRIOR APPLICATION NUMBER: US 10/350,555
;     PRIOR FILING DATE: 2003-01-23
;     NUMBER OF SEQ ID NOS: 72
;     SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;     LENGTH: 109
;     TYPE: PRT
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION:
;     OTHER INFORMATION: Description of Artificial Sequence:native cloned
;     OTHER INFORMATION: hybridoma murine 2D12.5 light chain variable
; US-10-625-047-22
;     OTHER INFORMATION: region (VL)

Query Match             92.9%;  Score 535;  DB 17;  Length 109;
Best Local Similarity   93.6%;  Pred. No. 2.6e-42;
Matches 102;  Conservative  1;  Mismatches  6;  Indels  0;  Gaps  0;

Qy         2 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVP 61
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNNRPPGVP 60

Qy        62 ARFSGSLIGDKAALTTISPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRVPGVP 110
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTRLTVLG 109
```

```
;     APPLICANT: The Regents of the University of California
;     TITLE OF INVENTION: Multi-Functional Antibodies
;     FILE REFERENCE: 023070-13091OUS
;     CURRENT APPLICATION NUMBER: US/10/625,047
;     CURRENT FILING DATE: 2003-07-22
;     PRIOR APPLICATION NUMBER: US 10/350,555
;     PRIOR FILING DATE: 2003-01-23
;     NUMBER OF SEQ ID NOS: 72
;     SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;     LENGTH: 218
;     TYPE: PRT
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION:
;     OTHER INFORMATION: Description of Artificial Sequence:native cloned
;     OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
;     OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
; US-10-625-047-27
;     OTHER INFORMATION: kappa light chain constant region (TTCL)

Query Match             92.4%;  Score 532;  DB 17;  Length 218;
Best Local Similarity   94.4%;  Pred. No. 1e-41;
Matches 102;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy         2 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVP 61
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         3 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNNRPPGVP 62

Qy        62 ARFSGSLIGDKAALTTISPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRVPGVP 109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        63 ARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVL 110

RESULT 9
US-10-625-047-23
; Sequence 23, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
;     APPLICANT: Meares, Claude
;     APPLICANT: Corneillie, Todd
;     APPLICANT: The Regents of the University of California
;     TITLE OF INVENTION: Multi-Functional Antibodies
;     FILE REFERENCE: 023070-13091OUS
;     CURRENT APPLICATION NUMBER: US/10/625,047
;     CURRENT FILING DATE: 2003-07-22
;     PRIOR APPLICATION NUMBER: US 10/350,555
;     PRIOR FILING DATE: 2003-01-23
;     NUMBER OF SEQ ID NOS: 72
;     SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;     LENGTH: 109
;     TYPE: PRT
;     ORGANISM: Artificial Sequence
;     FEATURE:
;     OTHER INFORMATION:
;     OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
;     OTHER INFORMATION: mutant murine 2D12.5 light chain variable region
; US-10-625-047-23
;     OTHER INFORMATION: (VL)

Query Match             92.2%;  Score 531;  DB 17;  Length 109;
Best Local Similarity   94.4%;  Pred. No. 6.2e-42;
Matches 102;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy         2 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVP 61
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNNRPPGVP 60

Qy        62 ARFSGSLIGDKAALTTISPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTINRVPGVP 61
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVL 108

RESULT 10
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```
RESULT 8
US-10-625-047-27
; Sequence 27, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
;     APPLICANT: Meares, Claude
;     APPLICANT: Corneillie, Todd
```

US-10-625-047-28
; Sequence 28, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Corneillie, Todd
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-1309100US
; CURRENT APPLICATION NUMBER: US/10/625,047
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 28
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
; OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
; OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
; OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-625-047-28

Query Match   92.2%;   Score 531; DB 17; Length 218;
Best Local Similarity 94.4%; Pred. No. 1.3e-41;
Matches 102; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   2 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVP 61
          ||||||||||||||||||||||||||||||| ||||||||||||||||||| |||||
Db   3 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPGVP 62

Qy   62 ARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL 109
          |||||||||||||||| || ||||||||||||||||||||||||||||
Db   63 ARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVL 110

RESULT 11
US-09-865-483-7
; Sequence 7, Application US/0986548...
; Patent No. US20020615881A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SU
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/09/865,483
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-865-483-7

Query Match   93.6%;   Score 530.5; DB 9; Length 109;
Best Local Similarity 92.1%; Pred. No. 6.9e-42;
Matches 103; Conservative   3; Mismatches   3; Indels   1; Gaps   1;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||: ::||||||||||||||:|||||:|||:
Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAITTNNFANWVQEKPDHLFTGLIGDTNNRVPGV 60

Qy   61 PARFSGSSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||||||||||||||||||||||||||||| : |||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWY-NNWVFGGGTKLTVLG 109

; Sequence 7, Application US/10726555
; Publication No. US20040191259A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SU
; TITLE OF INVENTION: ANTIGEN AND A GENE ENCODING THE SAME
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/10/726,555
; PRIOR APPLICATION NUMBER: US/09/865,483
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-726-555-7

Query Match   93.6%;   Score 530.5; DB 17; Length 109;
Best Local Similarity 92.1%; Pred. No. 6.9e-42;
Matches 103; Conservative   3; Mismatches   3; Indels   1; Gaps   1;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
          |||||||||||||||||||||||||||||: ::||||||||||||||:|||||:|||:
Db   1 QAVVTQESALTTSPGETVTLTCRSSTGAITTNNFANWVQEKPDHLFTGLIGDTNNRVPGV 60

Qy   61 PARFSGSSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          ||||||||||||||||||||||||||||||||||:: ||||||||||||||
Db   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWY-NNWVFGGGTKLTVLG 109

RESULT 13
US-10-305-268-4
; Sequence 4, Application US/10305268
; Publication No. US20030124057A1
; GENERAL INFORMATION:
; APPLICANT: GRIFFITHS, GARY L.
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GOVINDAN, SERENGULAM V.
; APPLICANT: LOSMAN, MICHELLE
; APPLICANT: QU, ZHENGXING
; TITLE OF INVENTION: ANTI-DOTA ANTIBODY
; FILE REFERENCE: 18733/1154
; CURRENT APPLICATION NUMBER: US/10/305,268
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/333,479
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-305-268-4

Query Match   92.0%;   Score 530; DB 14; Length 108;
Best Local Similarity 92.6%; Pred. No. 7.6e-42;
Matches 100; Conservative   5; Mismatches   3; Indels   0; Gaps   0;

Qy   3 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGVP 62
          |||||||||||||||||||||||||||||:::||||||||||||||:|||||:|||:
Db   1 VVTQESALTTSPGETVTLTCRSSSGAVTTNNYANWVQEKPDHLFTGLIGDTNNRAPGVPA 60

Qy   63 RFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
          |||||||||||||||||||||||||||||||:| : |||||||||||
Db   61 RFSGSLIGDKAALTITGAQTEDEAIYFCALWFSDHWVFGGGTELTVLG 108

RESULT 14

US-10-328-190-14
; Sequence 14, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND A.
; APPLICANT: CHANG, CHIEN-HSING KEN
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
; TITLE OF INVENTION: FROM VH AND VL DOMAINS
; FILE REFERENCE: 042418/0115
; CURRENT APPLICATION NUMBER: US/10/328,190
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/342,103
; PRIOR FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 14
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein
; OTHER INFORMATION: sequence for VL-chain of TS1
US-10-328-190-14

Query Match   90.6%; Score 522; DB 14; Length 391;
Best Local Similarity 90.0%; Pred. No. 1.7e-40;
Matches 99; Conservative   2; Mismatches   9; Indels   0; Gaps   0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
           |||||||||||||||||||||||||||| | |||||||| ||||||||||||||||||||
Db   152 QTVVTQESALTTSPGETVTFTCRSSAGAVTISNYANWVQEKPDHLFSGLIGGTTNRAPGV 211

Qy   61 PARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   212 PARFSGSLIGDKAALTITGAQTEDEAIYFCVLWYSDRWVFGGGAKLTVLG 261

RESULT 15
US-10-768-193-8
; Sequence 8, Application US/10768193
; Publication No. US20040181042A1
; GENERAL INFORMATION:
; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
; APPLICANT: The director of Chubu National Hospital
; APPLICANT: YANAGISAWA, Katsuhiko
; APPLICANT: SHIBATA, Masao
; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
; TITLE OF INVENTION: amyloid b-protein and DNA encoding the antibody
; FILE REFERENCE: P0102402
; CURRENT APPLICATION NUMBER: US/10/768,193
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: JP P2001-235700
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/JP02/07874
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 8
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-768-193-8

Query Match   90.1%; Score 519; DB 16; Length 129;
Best Local Similarity 90.0%; Pred. No. 9.7e-41;
Matches 99; Conservative   4; Mismatches   7; Indels   0; Gaps   0;

Qy   1 QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNSANWVQEKPDHLFTGLIGGTINRVPGV 60
           |||||||||||||||||||||||||||||||| | |||||||| |||||||||||:||||
Db   20 QAVVTQESALTTSPGGTVILTCRSSTGAVTISNYANWVQBKPDHLFTGLIGGTISNRAPGV 79

Qy   61 PARFSGSLIGDKAALTITGAQTEDEALYFCALWYSNHWVFGGGTKLTVLG 110
           ||||||||||||||||||||||||||||:||||||||||||||||||||||
Db   PARFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129

Db   80 PVRFSGSLIGDKAALTITGAQTEDDAMYFCALWYSTHYVFGGGTKVTVLG 129

Search completed: December 29, 2004, 18:42:00
Job time : 64.5988 secs

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                                    GenCore version 5.1.6

                                    Copyright (c) 1993 - 2004 Compugen Ltd.


OM protein - protein search, using sw model

Run on:           December 29, 2004, 17:38:43 ; Search time 80.0708 seconds
                                                (without alignments)
                                                833.556 Million cell updates/sec

Title:            US-10-774-076-4
Perfect score:    617
Sequence:         1 EVQLQQSGAELVRSGASVKL..........YGGTITFAYWGQGTLVTVSA 116

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:          1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        UniProt_02:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

Result                 Query
 No.    Score    Match Length DB  ID        Description
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  1     489.5    79.3   468    2  Q99L31    Q99L31 mus musculu
  2     439.5    71.2   109    2  Q9JL85    Q9JL85 mus musculu
  3     413.5    67.0   473    2  Q9D8L4    Q9D8L4 mus musculu
  4     408.5    66.2   614    2  Q7TMT6    Q7TMT6 mus musculu
  5     407      66.0   139    2  Q924R5    Q924R5 mus musculu
  6     407      66.0   465    2  Q6PJB2    Q6PJB2 mus musculu
  7     407      66.0   465    2  AAH18280  AAH18280 mus muscu
  8     403.5    65.4   120    2  HV03_MOUSE  P01747 mus musculu
  9     401      65.0   118    2  Q9ZIC4    Q9ZIC4 mus musculu
 10     401      65.0   139    1  HV07_MOUSE  P01751 mus musculu
 11     401      65.0   145    2  Q924Q7    Q924Q7 mus musculu
 12     400.5    64.9   140    1  HV02_MOUSE  P01746 mus musculu
 13     400      64.8   136    2  Q7TPE3    Q7TPE3 mus musculu
 14     398      64.5   146    2  Q924R1    Q924R1 mus musculu
 15     397.5    64.4   146    2  Q924R8    Q924R8 mus musculu
 16     396      64.2   124    2  Q9UL92    Q9UL92 homo sapien
 17     394      63.9   145    2  Q924Q6    Q924Q6 mus musculu
 18     394      63.9   145    2  Q924Q9    Q924Q9 mus musculu
 19     394      63.9   473    2  Q99L25    Q99L25 mus musculu
 20     392.5    63.6   142    2  Q924R2    Q924R2 mus musculu
 21     392.5    63.6   142    2  Q924Q1    Q924Q1 mus musculu
 22     392      63.5   143    2  Q924P9    Q924P9 mus musculu
 23     391      63.4   143    2  Q91V67    Q91V67 mus musculu
 24     391      63.4   145    2  Q924R4    Q924R4 mus musculu
 25     390.5    63.3   142    2  Q924Q2    Q924Q2 mus musculu
 26     390      63.2   141    2  Q924Q4    Q924Q4 mus musculu
 27     390      63.2   145    2  Q924R3    Q924R3 mus musculu
 28     390      63.2   488    2  Q91WR1    Q91WR1 mus musculu
 29     389.5    63.1   146    2  Q924R3    Q924R3 mus musculu
 30     389.5    63.1   489    2  Q8VCX4    Q8VCX4 mus musculu
 31     389      63.0   143    2  Q924R0    Q924R0 mus musculu
 32     389      63.0   145    2  Q924P7    Q924P7 mus musculu
 33     389      63.0   482    2  Q8K172    Q8K172 mus musculu
 34     387.5    62.8   481    2  Q91WT1    Q91WT1 mus musculu
 35     387      62.7   137    2  Q924R6    Q924R6 mus musculu
 36     386.5    62.6   146    2  Q924Q8    Q924Q8 mus musculu
 37     385.5    62.5   472    2  Q6PJA7    Q6PJA7 mus musculu
 38     385.5    62.5   472    2  AAH18535  AAH18535 mus muscu
 39     384.5    62.3   144    2  Q924P5    Q924P5 mus musculu
 40     384.5    62.3   464    2  Q924R7    Q924R7 homo sapi
 41     384      62.2   143    2  Aah19337  Aah19337 homo sapi
 42     384      62.2   143    2  Q99LC4    Q99LC4 mus musculu
 43     383.5    62.2   480    2  Q6P089    Q6P089 mus musculu
 44     383.5    62.2   480    2  Aah65733  Aah65733 homo sapi
 45     383      62.1   613    2  Q8VCX7    Q8VCX7 homo musculu

                               ALIGNMENTS

RESULT 1
ID   Q99L31
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
DR   PDB; 1A3R; X-ray; H=-.
DR   PDB; 2AP2; X-ray; B/D=20-139.
DR   PDB; 1A3R; X-ray; H=20-139.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR013106; Ig_MHC.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
```

RESULT 1

Q99L31   PRELIMINARY;   PRT;   468 AA.

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DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   468 AA;  51661 MW;  9635232B33332ADB CRC64;

Query Match             79.3%;  Score 489.5;  DB 2;  Length 468;
Best Local Similarity   78.5%;  Pred. No. 2.3e-41;
Matches    95;  Conservative  10;  Pred.  No.  9;  Mismatches  9;  Indels  7;  Gaps  2;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY   60
            :|||||||||||| ||||||||||||||||   :|||||||||||||| :||:|:|
Db    1  EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMIWVKQRPEQGLEWIGWIDPEDGETKY   60

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVS  115
            |:||| :|||||||||||||||||||||||||      || ||||||||| :||||
Db   80  APKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLLYGG--YDYWGQGTTITVS  137

Qy  116  A  116
Db  138  S  138
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RESULT 2
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ID   Q9JL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Maikiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206021; AAF69319.1; -.
DR   HSSP; Q99L3I; 2AP2.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1      1
FT   NON_TER      109    109
SQ   SEQUENCE   109 AA;  11944 MW;  DFE615FB6CED4EDE CRC64;

Query Match             71.2%;  Score 439.5;  DB 2;  Length 109;
Best Local Similarity   76.1%;  Pred. No. 5.5e-37;
Matches    83;  Conservative  11;  Mismatches  14;  Indels  1;  Gaps  1;

Qy    9  AELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYAPNFQGRA   68
            ||||:|||||||||||||||||||||| :|||||||||||||:|||:||:|
Db    1  AELVRPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA   60

Qy   69  TMTADTSSNTAYLQLSSLTSEDTAVYYCY-GGTITFAYWGQGTLVTVSA  116
            |:||||||||||||||||||||||| :||||||||||||:|||
Db   61  TITSDTSSNTAYLQLSSLTSEDTAVYYCVRRGAVVFDYWGQGTALTVSS  109
```

RESULT 3
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ID   Q9D8L4      PRELIMINARY;      PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE   library, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy
DE   chain of IgM), full insert sequence.
GN   Name=Igh-1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=99279253; PubMed=10349636;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RG   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20499374; PubMed=11042159;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=20530913; PubMed=11076861;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Itoh M.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK007916; BAB25349.1; -.
DR   PIR; PH1165; PH1165.
DR   PIR; S19966; S19966.
DR   PIR; S26746; S26746.
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DR   HSSP; P01864; 1BOG.
DR   MGD; MGI:96443; Igh-1a.
DR   GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR   GO; GO:0005771; C:multivesicular body; IDA.
DR   GO; GO:0003823; F:antigen binding; IDA.
DR   GO; GO:0001788; F:antibody-dependent cellular cytotoxicity; IDA.
DR   GO; GO:0003333; P:antigen processing; IDA.
DR   GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR   GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR   GO; GO:0006911; P:endosome to lysosome transport; IDA.
DR   GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR   GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR   GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR   GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR   GO; GO:0050778; P:positive regulation of immune response; IDA.
DR   GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR   GO; GO:0001798; P:positive regulation of type IIa hypersensi...; IDA.
DR   GO; GO:0003162; P:regulation ....;
DR   GO; GO:0001798; P:positive regulation of proteolysis and peptidolysis; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

Query Match             67.0%;  Score 413.5;  DB 2;  Length 473;
Best Local Similarity   68.1%;  Pred. No. 1.3e-33;
Matches   81;  Conservative   14;  Mismatches   21;  Indels   3;  Gaps   1;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
         ||||| :|||||||:|||||:| ||||||||||||||||||| |:||||||| | | |||
Db   20  QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTY   79

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTIP---FAYWGQGTLVTVSA  116
         :| |:| ||:||| |||||||| ||||||:||| | ||||:      |:|:|||||:||
Db   80  NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA  138
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RESULT 4

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ID   Q7TMT6
AC   Q7TMT6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   MGC60843 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC053409; AAH53409.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   614 AA;  67746 MW;  839BAF3B8D124F89 CRC64;

Query Match             66.2%;  Score 408.5;  DB 2;  Length 614;
Best Local Similarity   65.5%;  Pred. No. 5.8e-33;
Matches   78;  Conservative   18;  Mismatches   20;  Indels   3;  Gaps   1;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
         :||||||| ||||:|||||:| ||||  :  ::: ||||||| :|||||||| | | |||
Db   20  QVQLQQSGPELVKPGASVKVSCKASGYAFSSSWMNWVKQRPGKGLEWIGRVYPGDGDTNY  79

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSBDTAVYYC---YGGTITFAYWGQGTLVTVSA  116
         :  | |:||:||| |||||||| ||||||:||| |    | |  :||||||||||:||
Db   80  NGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDYGSSYRFAYWGQGTLVTVSA  138
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RESULT 5

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ID   Q924R5
AC   Q924R5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067784; BAB63269.1; -.
PIR; PH1137; PH1137.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1      1
FT   NON_TER      139    139
SQ   SEQUENCE   139 AA;  15221 MW;  8491B2F85614736A CRC64;

Query Match             66.0%;  Score 407;  DB 2;  Length 139;
Best Local Similarity   67.2%;  Pred. No. 1.5e-33;
Matches   78;  Conservative   14;  Mismatches   22;  Indels   2;  Gaps   1;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
         :||||| ||||||:|||||||| ||||| : : ||:||||||| :|||||| | | : ||
Db    1  QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY  60

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA  116
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Db

RESULT 6
ID   Q6PJB2
AC   Q6PJB2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
SQ   SEQUENCE 465 AA; 394F43C4B8DB3E21 CRC64;

Qy   61 NEKFPKSRATLIVDKPSSTAYMQLSSLTSEDSAVYYC--ALLAEAYWGQGTLVTVSA 114
              ||||||||:||:||||||||:|||||||||||||||| :||||:||||||||||||||
Db   80 NEKFPKGRATLTPADKSSSTAYMELSSLTSEDSAVYYCARGRYYVFDYWGQGTTITVSS 135

Query Match   66.0%; Score 407; DB 2; Length 465;
Best Local Similarity   65.5%; Pred. No. 6e-33;
Matches   76; Conservative   15; Mismatches 25; Indels   0; Gaps   0;

Qy   1 EVQLQQSGAELVRGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
              :|||||:|||||||||||||||||||||::||:|||||||||||||||||:|||||||||
Db   20 QVQLKQSGAELVKPGASVKLSCKASGYTFNSYIMHWVKQRPGQGLEWIGYFSPYNDDTKC 79

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
              :||:|:|||::||||::|||||||||||||::|||||||:||:||||||||:||||:
Db   80 NEKFPKGRATLTPADKSSSTAYMELSSLTSEDSAVYYCARGRYYVFDYWGQGTTITVSS 135

RESULT 7
ID   AAH18280
AC   AAH18280;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary tumor;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary tumor;
RL   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RA   EMBL; BC018280; AAH18280.1; -.
DR   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
KW   Hypothetical protein.
SQ   SEQUENCE 465 AA; 394F43C4B8DB3E21 CRC64;

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
              :||:|:|||::||||::|||||||||||||::|||||||:||:||||||||:||||:
Db   80 NEKFPKGRATLTPADKSSSTAYMELSSLTSEDSAVYYCARGRYYVFDYWGQGTTITVSS 135

Query Match   66.0%; Score 407; DB 2; Length 465;
Best Local Similarity   65.5%; Pred. No. 6e-33;
Matches   76; Conservative   15; Mismatches 25; Indels   0; Gaps   0;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
              :|||||:||||||:||||||||||||||::||:|||||||||||||||||:|||||||||
Db   20 QVQLKQSGAELVKPGASVKLSCKASGYTFNSYIMHWVKQRPGQGLEWIGYFSPYNDDTKC 79

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
              :||:|:|||::||||::|||||||||||||::|||||||:||:||||||||:||||:
Db   80 NEKFPKGRATLTPADKSSSTAYMELSSLTSEDSAVYYCARGRYYVFDYWGQGTTITVSS 135

RESULT 8
ID   HV03_MOUSE
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: From analysis of the sizes of several other
CC       differentiated genes that hybridize to this one, the authors
CC       conclude that all of these V regions have rearranged to the same J
CC       segment, JH2.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PDB; 1JFQ; X-ray; H=1-120.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1    120       Ig-like.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04B4A167B654AF CRC64;
```

Query Match
Best Local Similarity 64.2%; Pred. No. 2.9e-33;
Matches 77; Conservative 17; Mismatches 21; Indels 5; Gaps 1;

```
Qy   2  VQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYA  61
        |||:||||||||.|.:.|| ||||||...:.|.|:|:||||||.|||||||| : :.|.:
Db   1  VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN  60

Qy  62  PNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTIFPAYWGQGTLVTVSA  116
        ..::|.:||:.|.:|||||:||.||||||:|||:|     ||:::||.:||||||.||||
Db  61  EKPKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYFPDYWGQGTTLTVSS  120
```

Query Match
Best Local Similarity 65.4%; Score 403.5; DB 1; Length 120;
Matches 77; Conservative 17; Mismatches 21; Indels 5; Gaps 1;

RESULT 9
Q92IC4

```
ID   Q92IC4      PRELIMINARY;      PRT;   118 AA.
AC   Q92IC4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Balb/c;
RX   MEDLINE=97450619; PubMed=9307060;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott B.A., Squinto S.P.,
RA   Matis L.A., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Mol. Immunol. 34:441-452(1997).
DR   EMBL; U78801; AAD00293.1; -.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   118 AA;  13036 MW;  90EC559D31EC4FC CRC64;
```

Query Match
65.0%; Score 401; DB 2; Length 118;

Best Local Similarity 65.3%; Pred. No. 5.1e-33;
Matches 77; Conservative 15; Mismatches 24; Indels 2; Gaps 1;

```
Qy   1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
        :|||||||||. .:..||||||.|||.|.|:|:|:.||||||.|||||||.|. .:.|.:
Db   1  QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY  60

Qy  61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTI--TFPAYWGQGTLVTVSA  116
        :..:.|.||:|||.|||||||||||:|||:||||||.. .:  :||.:||||||.||||
Db  61  TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYFPDYWGQGTTLTVSS  118
```

RESULT 10
HV07_MOUSE

```
ID   HV07_MOUSE   STANDARD;      PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region B1-8/186-2 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma
CC       making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
CC       (NPb antibodies).
```
```
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A90809; MHMS18.
DR   PDB; 1A90; X-ray; H=20-139.
DR   PDB; 1A6U; X-ray; H=20-139.
DR   PDB; 1A6V; X-ray; H/I/J=20-139.
DR   PDB; 1A6W; X-ray; H=20-139.
DR   PDB; 1NQB; X-ray; A/C=20-139.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    139       Ig heavy chain V region B1-8/186-2.
FT   DOMAIN       20     49       Framework-1.
FT   DOMAIN       50     54       Complementarity-determining-1.
FT   DOMAIN       55     68       Framework-2.
FT   DOMAIN       69     85       Complementarity-determining-2.
FT   DOMAIN       86    117       Framework-3.
FT   DOMAIN      118    124       D segment.
FT   DOMAIN      125    139       JH2 SEGMENT.
FT   DISULFID     41    115       By similarity.
FT   STRAND       22     24
FT   STRAND       28     31
FT   TURN         33     34
FT   STRAND       37     44
FT   STRAND       48     50
FT   HELIX        52     58
FT   STRAND
```

```
FT   TURN          60     61
FT   STRAND        64     70
FT   TURN          72     74
FT   TURN          77     79
FT   HELIX         81     83
FT   HELIX         84     86
FT   NON_TER       87     92
FT   STRAND        93     96
FT   TURN          97    102
FT   HELIX        107    109
FT   STRAND       111    118
FT   TURN         120    123
FT   STRAND       129    129
FT   STRAND       133    137
FT   NON_TER      139    139
SQ   SEQUENCE     139 AA;  15419 MW;  1B57DD4FD0C9F465 CRC64;

Query Match         65.0%;  Score 401;  DB 1;  Length 139;
Best Local Similarity 63.3%;  Pred. No. 6.2e-33;
Matches  76;  Conservative  17;  Mismatches  23;  Indels  4;  Gaps  1;

Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY   60
         :|||||||:||||:|||||||||:|:||:|||||||||||||||||||:|||||::|:
Db   20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY   79

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVSA  116
         :||||:|:|:|||:||||||||||||||||:|||||     :||||||||||||:||:
Db   80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTLTVSS  139
```

RESULT 11

```
ID   Q92AQ7       PRELIMINARY;    PRT;   145 AA.
AC   Q92AQ7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067793; BAB63278.1; -.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.

Query Match         65.0%;  Score 401;  DB 1;  Length 145;
Best Local Similarity 63.3%;  Pred. No. 6.5e-33;
Matches  76;  Conservative  17;  Mismatches  23;  Indels  4;  Gaps  1;

Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY   60
         :|||||||:||||:|||||||||:|:||:|||||||||||||||||||:|||||::|:
Db    1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY   60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVSA  116
         :||||:|:|:|||:||||||||||||||||:|||||     :||||||||||||:||:
Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTLTVSS  120
```

RESULT 12

```
ID   HV02_MOUSE   STANDARD;    PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A94264; HVMSG7.
DR   HSSP; P01747; 1JFQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    140       Ig heavy chain V region 93G7.
FT   DOMAIN       20    139       Ig-like.
FT   NON_TER     140    140
SQ   SEQUENCE    140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;

Query Match         64.9%;  Score 400.5;  DB 1;  Length 140;
Best Local Similarity 63.6%;  Pred. No. 7e-33;
Matches  77;  Conservative  16;  Mismatches  23;  Indels  5;  Gaps  1;

Qy    1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY   60
         |||||||||||:||||:|:||||:||:|||     ||||||||:|||||||:|:|:
Db   20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY   79
```

```
Qy    61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVS 115
            ||| |||||:||||||||||||||||||:|||:|            |||||||||:|||
Db    80 NBKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYGGSYDFDYWGQGTPLTVS 139

Qy   116 A 116
           |
Db   140 S 140
```

RESULT 13
Q7TPB3
ID   Q7TPB3   PRELIMINARY;   PRT;   136 AA.
AC   Q7TPB3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Psuedo gene (Fragment).
GN   Name=V23-D-J-IgG1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB069864; BAC54573.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   136   136
SQ   SEQUENCE   136 AA; 14882 MW; 99392B1A31F663AF CRC64;

Query Match   64.8%; Score 400; DB 2; Length 136;
Best Local Similarity   65.8%; Pred. No. 7.6e-33;
Matches   77; Conservative 12; Mismatches 24; Indels   4; Gaps   1;

```
Qy     4 LQGSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYAPN 63
           |:||:||:||||||||||:||||||||||||||||||:|||||||||||||||| :
Db     1 LQQPGTELVKPGASVKLSCQASGYTFTSFWMHWVKQRPGQGLEWIGNIYPSNGDTNYNEK 60

Qy    64 FQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVSA 116
           | |:|||||||||||||||:||||||||||||         |:|||||||||||||||
Db    61 FKSKATLTVDKXSSTAYMQLSSLTSEDSAVYYCTRKDYGSSGFVIWGQGTLVTVSA 117
```

DR   PIR; PHl108; PHl108.
DR   PIR; PHl114; PHl114.
DR   PIR; PHl118; PHl118.
DR   PIR; PHl119; PHl119.
DR   PIR; PHl125; PHl125.
DR   PIR; PHl126; PHl126.
DR   PIR; PHl128; PHl128.
DR   PIR; PHl129; PHl129.
DR   PIR; PHl131; PHl131.
DR   PIR; PHl134; PHl134.
DR   PIR; PHl137; PHl137.
DR   PIR; PHl139; PHl139.
DR   PIR; PHl142; PHl142.
DR   PIR; PHl144; PHl144.
DR   PIR; PHl147; PHl147.
DR   PIR; PHl149; PHl149.
DR   PIR; PHl150; PHl150.
DR   PIR; PHl151; PHl151.
DR   PIR; PHl152; PHl152.
DR   PIR; PHl153; PHl153.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   145   145
SQ   SEQUENCE   145 AA; 15979 MW; 0162D0A26C7746C04 CRC64;

Query Match   64.5%; Score 398; DB 2; Length 145;
Best Local Similarity   64.2%; Pred. No. 1.3e-32;
Matches   77; Conservative 17; Mismatches 22; Indels   4; Gaps   2;

```
Qy     1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
           :|||||:||:||||||||||:||||||||||||||||||:||||||||||||||| :
Db     1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

Qy    61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITFA--YWGQGTLVTVSA 116
           |||||| |:||||||||||||||:|||||||||||        |:|||    |||||||||:|
Db    61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDGSSFYAMDYWGQGTSVTVSS 120
```

RESULT 14
Q924R1
ID   Q924R1   PRELIMINARY;   PRT;   145 AA.
AC   Q924R1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067789; BAB63274.1; -.
DR   PIR; F28833; F28833.
DR   PIR; F33932; F33932.
DR   PIR; PHl105; PHl105.

RESULT 15
Q924R8
ID   Q924R8   PRELIMINARY;   PRT;   146 AA.
AC   Q924R8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067781; BAB63266.1; -.
DR   PIR; F28833; F28833.

DR   PIR; PHl108; PHl108.
DR   PIR; PHl114; PHl114.
DR   PIR; PHl118; PHl118.
DR   PIR; PHl119; PHl119.
DR   PIR; PHl125; PHl125.
DR   PIR; PHl126; PHl126.
DR   PIR; PHl128; PHl128.
DR   PIR; PHl129; PHl129.
DR   PIR; PHl131; PHl131.
DR   PIR; PHl134; PHl134.

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DR   PIR; PH1137.
DR   PIR; PH1139; PH1137.
DR   PIR; PH1142.
DR   PIR; PH1144; PH1142.
DR   PIR; PH1144.
DR   PIR; PH1147;
DR   PIR; PH1147;
DR   PIR; PH1149;
DR   PIR; PH1149;
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151.
DR   PIR; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   PIR; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1
FT   NON_TER       1
SQ   SEQUENCE    146 AA;  16216 MW;  92460F1FDF1B7538 CRC64;

Query Match             64.4%;  Score 397.5;  DB 2;  Length 146;
Best Local Similarity   62.8%;  Pred. No. 1.5e-32;
Matches   76;  Conservative  18;  Mismatches  22;  Indels  5;  Gaps  2;

Qy      1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY   60
          :|||:|| ||||||: :|||||||:  :||:|:.  |:|||||||||:||| :|:|:|
Db      1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY   60

Qy     61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTI-TFAYWGQGTLVTVS  115
          | :|:|:|||:|:|:|||||:|||||||:||||||||    | ::  ||||||||||||
Db     61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSYYGSSLYYFDYWGQGTTLTVS  120

Qy    116 A 116
          :
Db    121 S 121
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Search completed: December 29, 2004, 18:05:18
Job time : 80.0708 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 15.9115 Seconds
                 (without alignments)
                 701.451 Million cell updates/sec

Title: US-10-774-076-4
Perfect score: 617
Sequence: 1 EVQLQQSGAELVRSGASVKL..........YGGTITPAYWGQGTLVTVSA 116

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR 79:*
                 1: piri:*
                 2: piri:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	516.5	83.7	118	2	S25174	Ig heavy chain V r
2	500.5	81.1	136	2	S04576	Ig heavy chain V r
3	500	81.0	137	2	S52445	Ig heavy chain V r
4	493	79.9	178	2	S29594	Ig gamma chain (WM
5	487.5	79.0	120	2	S03471	Ig heavy chain V-D
6	478	77.5	120	2	S15672	Ig heavy chain V r
7	474.5	76.9	117	2	S17586	Ig heavy chain V r
8	474	76.8	122	2	S06823	Ig heavy chain V r
9	470.5	76.3	115	2	S03482	Ig heavy chain V-D
10	460.5	74.6	221	2	S49220	Ig gamma-1 chain
11	456.5	74.0	120	2	S03484	Ig heavy chain V-D
12	453.5	73.5	107	2	PH1013	Ig heavy chain V r
13	453	73.4	268	2	A56446	Ig gamma chain V r
14	451.5	73.2	116	2	S24289	Ig gamma chain V r
15	446.5	72.4	233	2	JC5322	p53 specific singl
16	446	72.3	108	2	PH1012	Ig heavy chain V r
17	446	72.3	115	2	PL0246	Ig heavy chain V r
18	443	71.8	123	2	PH1403	Ig heavy chain V r
19	442	71.6	118	2	G37267	Ig heavy chain V r
20	439	71.2	114	4	A47271	nitrophenyl phosph
21	436.5	70.7	249	2	S41374	single chain Fv an
22	428	69.4	288	2	S29690	single chain Fv an
23	426.5	69.1	119	2	E30562	Ig heavy chain VDJ
24	426.5	69.0	119	2	D30562	Ig heavy chain V r
25	424.5	68.8	119	2	C30562	Ig heavy chain V r
26	424.5	68.8	119	2	S21810	Ig heavy chain V r
27	422.5	68.5	138	2	S21810	Ig heavy chain V r
28	420.5	68.2	246	2	S40295	Ig gamma-2a chain
29	420.5	68.2	446	2	S40295	Ig gamma chain - m
29	416	67.4	107	2	A27646	Ig heavy chain V r
30	413	66.9	120	2	S41394	Ig heavy chain V r
31	410	66.5	469	2	S37483	Ig gamma-2a chain
32	408.5	66.2	140	2	PH1482	Ig heavy chain V r
33	406.5	65.9	117	2	JC2269	PL7-6 antibody hea
34	406	65.8	137	2	E29380	Ig heavy chain pre
35	403	65.3	118	2	C30560	Ig heavy chain V r
36	403	65.3	139	2	P90024	Ig heavy chain pre
37	402	65.2	135	2	A30577	antibody Fab Je1
38	401	65.0	120	2	P22769	Ig heavy chain pre
39	401	65.0	139	1	MRMS18	Ig heavy chain V r
40	401	65.0	287	4	HVMSG7	pelB leader/Ig hea
41	401	65.0	116	2	PC4402	Ig heavy chain pre
42	400.5	64.9	140	1	G45722	pelB leader/Ig pre
43	399.5	64.7	117	2	S25175	anti-glycoprotein
44	399.5	64.7	120	2	S25175	Ig heavy chain V r
45	398.5	64.6	116	2	S55542	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S25174
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S25174; S33133
R;Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A;Description: Structure and binding properties of monoclonal antibodies to core histon...
A;Reference number: S25174
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
A;Accession: S33133
A;Cross-references: EMBL:X67622; NID:g51854; PIDN:CAA47880.1; PID:g938259
A;Accession: S25174
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <MON>
A;Accession: S25174
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <MO2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 516.5; DB 2; Length 118;
Best Local Similarity 84.7%; Pred. No. 5e-41;
Matches 100; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

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Qy  1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        |:|||||||||| |||||||||||||||| |:|||||||||||||||||| |||||||||
Db  1 EIQLQQSGAELVXXGASVKLSCTASGFNIKDDYLHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCVGGTI---TFAYWGQGTLVTVS 115
        |||||| ||:|||||||||||||||| |||||| |||||     :|||||||||||||
Db 61 ASKFQGKATITADTSSNTAYLQLSSLITSEDTRAVYYCSSPLVHLRTFAYWGQGTLVTVS 118
```

RESULT 2
S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; T...
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involvem...
A;Reference number: S04576
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g952030
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g952030
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```
             C;Keywords: heterotetramer; immunoglobulin
             F;1-19/Domain: signal sequence #status predicted <SIG>
             F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
             F;34-117/Domain: immunoglobulin homology <IMM>

Qy    Query Match
      Best Local Similarity   81.1%;  Score 500.5; DB 2; Length 136;
      Matches  98; Conservative   4; Mismatches  14; Indels   1; Gaps   1;

Qy     1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
         |||||||||||||||||||||||||||||||||||||||:|||||||||:||||||||||
Db    20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRPEQGLEWIGWIDPENGDTQY 79

Qy    61 APNFQGRAATMTADTSSNTAYLQLSSLTSEDTAVYYCYG-GTIIFAYWGQGTLVTVSA 116
         ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    80 ASKFQGKATMTADTSSNTTYLQLSSLTSEDTAVYYCTTYGAYAMDYWGQGTSVTVSS 136


RESULT 3
S52445
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
R;Berdoz, J.; Kraehenbuhl, J.P.
A;Accession: S52445
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
submitted to the EMBL Data Library, November 1994
EMBO J. 2, 867-872, 1983
A;Reference number: S52445
A;Accession: S52445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:G673439; PIDN:CAA58011.1; PID:g673440
C;Genetics:
C;Introns: 16/1
C;Superfamily: immunoglobulin; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>

Qy    Query Match
      Best Local Similarity   81.0%;  Score 500; DB 2; Length 137;
      Matches  97; Conservative   7; Mismatches  12; Indels   2; Gaps   1;

Qy     1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
         ||||||||||||||||||||||||||||||||:|||||||||:||||||||||:|||||
Db    20 EVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYMVKVKQRPEQGLEWIGWIDPENGNTVY 79

Qy    61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTIIFPAYWGQGTLVTVSA 116
         |||||||||||||||||||||||||||||||||:  ||:|:|||||||||||||||||
Db    80 DPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCAYGTSYWPFYWGQGTLVTVSA 137


RESULT 4
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
R;Seymour, R.
A;Accession: S29594
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Qy    Query Match
      Best Local Similarity   79.9%;  Score 493; DB 2; Length 178;
      Matches  95; Conservative   8; Mismatches  13; Indels   2; Gaps   1;

Qy     1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
```

```
Db    14 EVQLQQSGAELVRPGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGRIDPANGYTEY 73

Qy    61 APNFQGRAATMTADTSSNTAYLQLSSLTSEDTAVYYCYG-GTIIFPA--YWGQGTLVTVSA 116
Db    74 DPKFQGKATITADTSNTAYLQLSSLTSEDTAVYYCTCYGGNYAYGMDYWGQGTSVTVSS 131


RESULT 5
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
A;Residues: 7-120 <ROC1>
A;Molecule type: mRNA
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fouger
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not s
A;Reference number: S07453; MUID:83050821; PMID:6815271
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Qy    Query Match
      Best Local Similarity   79.0%;  Score 487.5; DB 2; Length 120;
      Matches  95; Conservative   8; Mismatches  13; Indels   3; Gaps   1;

Qy     1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
Db     1 EVQLQQSGAELVRPGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy    61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTIIFPAYWGQGTLVTVSA 116
Db    61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGWLRRDAMDYWGQGTSVTVSS 119


RESULT 6
S15672
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
R;Tempest, P.R.; Brenner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,
Bio/Technology 9, 266-271, 1991
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial vi
A;Reference number: S15672; MUID:91337412; PMID:1367535
A;Accession: S15672
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-116 <TEM>
A;Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Qy    Query Match
      Best Local Similarity   77.5%;  Score 478; DB 2; Length 116;
      Matches  90; Conservative   9; Mismatches  16; Indels   0; Gaps   0;

Qy     2 VQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYA 61
```

Db   62 PKFQGRATMTADTSSNTAYLQLTSLTFEDTAVYFCNSWGGSDFDHWGQGTTLTVSS 116

Qy   62 VQLQKSGTELERSGASVKLSCTASGFNIKDYYMHWMKQRPDQGLEWIGWIDPENDVQYA 61

Db   2 VQLQKSGTELERSGASVKLSCTASGFNIKDYYMHWMKQRPDQGLEWIGWIDPENDVQYA 61

RESULT 7

S17586

Ig heavy chain V region (E8) - mouse (fragment)

C;Species: Mus musculus (house mouse)
A;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g518820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
A;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochrome
forms.
A;Reference number: S17586; MUID:92015240; PMID:1656053
A;Accession: S17586
A;Molecule type: mRNA
A;Status: preliminary

Query Match   76.9%; Score 474.5; DB 2; Length 117;
Best Local Similarity   77.5%; Pred. No. 3.9e-37;
Matches 93; Conservative 10; Mismatches 10; Indels 7; Gaps 2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
            |||||||||||||||||||||||||||||| :|||||:|: :||||||||| |||:||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDYYMHWVKQRPEKGLEWIGRIDPASGNTKY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITFAYWGQGTLVTV 114
            ||.||||||||||||||||||||||||||||||||||: ||||||||||||||||| :
Db   61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCAGYDYG---NFDYWGQGTTLTVSS 117

RESULT 8

S06823

Ig heavy chain V region (clone IIc) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
A;Accession: S06823
J. Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06823
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match   76.8%; Score 474; DB 2; Length 122;
Best Local Similarity   77.9%; Pred. No. 4.5e-37;
Matches 95; Conservative 8; Mismatches 13; Indels 6; Gaps 2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIH-WVKQRPEQGLEWIGCIDPENGDTE 59
            |||||||||||||||||||||||||||||||:|:|| |:||||||||||||| ||||:||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDYTMHEWVKQRPEQGLEWIGRIDPANGNTK 60

Qy   60 YAPNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCARGW----TITFAYWGQGTLVTV 114
            | |.||||||||||||||||||||||||||||||||||| || |||||||||||||||
Db   61 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGWLRRDAMGVDVWGQGTSVTV 120

RESULT 9

S03482

Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)

C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Accession: S03482; S07453
A;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GA
hypervariable regions.
A;Reference number: S03471; MUID:84057768; PMID:6416834
A;Accession: S03482
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fouge
J. Immunol 129, 255-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not s
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   76.3%; Score 470.5; DB 2; Length 115;
Best Local Similarity   79.1%; Pred. No. 8.9e-37;
Matches 91; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||:||||
Db   1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDYTMHWVKQRPEQGLEWIGRIDPAKGNTKY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-YGGTITFAYWGQGTLVTV 114
            |.||||||||||||||||||||||||||||||||||:|||||||||||||||||:
Db   61 DPKFQDKATITDTSSNTAYLQPSSLTSEDTAVYYCARGTTVGRDYWGQGTTLTV 115

RESULT 10

S49220

Ig gamma-1 chain - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A;Reference number: S49220
A;Accession: S49220
A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match   74.6%; Score 460.5; DB 2; Length 221;
Best Local Similarity   75.0%; Pred. No. 1.5e-35;
Matches 90; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
            :|:|||:|||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   1 QVKLLESGAELVKSGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGEIKY 60

Qy   115 SA 116
             |:
Db   121 SS 122

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITFAYWGQGTLVTVSA 116
          |||||| ||||||| |:|||||||||||||||||||| | || | |:|||||||
Db 61 DPKFQGTATITADTSTNTAYLQLSSLTSEDTAVYYCVARRGYGSS-QEPYWGQGTLLTVSS 119

RESULT 11
S03484
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03484; MUID:84057768; PMID:6416834
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021; PMID:6815271
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin; immunoglobulin homology
F;15-98/Domain: immunoglobulin V region; immunoglobulin homology <IMM>

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTITFAYWGQGTLVTVSA 116
          ||||| ||||||||||:||||||||||||||||||| ||| | ||:||||||
Db 61 GPKFQGKATITADTSSSAAYLQLSSLTSGDTAVYYCTRGWFRRDAMDYWGQGTSVTVSS 119

Query Match   74.0%;   Score 456.5; DB 2;   Length 120;
Best Local Similarity 75.6%;
Matches 90; Conservative 8; Mismatches 18; Indels 3; Gaps 1;

RESULT 12
PH1013
Ig heavy chain V region (clone 111.67) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1013
A;Molecule type: protein
A;Residues: 1-107 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1013
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA

Query Match   73.5%;   Score 453.5; DB 2;   Length 107;
Best Local Similarity 83.2%;   Pred. No. 3.1e-35;
Matches 89; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
         ||||||||||||| |||||||||||||||||||| ||||||||||||||| |||:|| |||
Db   1 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYIHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTI-TFAYW 106
          ||:||:|||||||||||||||||||||||||||||| :| || |
Db 61 APKFQDRATITADTSSNTAYLQLSSLTSEDTAVYYCARGSIWYFDVW 107

RESULT 13
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match   73.4%;   Score 453.;   DB 2;   Length 268;
Best Local Similarity 76.3%;   Pred. No. 9.2e-35;
Matches 90; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
         :|:||:||||||:|||||||||:||||||||| ||:||||||||||||||| |:|||| ||
Db   3 QVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGITKY 62

Qy 61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITFAYWGQGTLVTVSA 116
          ||:||:|||:||||||||||||||||||||||||||| | ||| ||:|||||||
Db 63 DPKFQGKATIAADTSSNTAYLQLSSLTSEDTAVYYCASYYLTRYENYWGQGTTVTVSS 120

RESULT 14
S24289
Ig gamma chain V region (J334/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
submitted to the EMBL Data library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of th
A;Reference number: S24287
A;Accession: S24289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:g951690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match   73.2%;   Score 451.5; DB 2;   Length 116;
Best Local Similarity 75.2%;   Pred. No. 5.2e-35;
Matches 88; Conservative 13; Mismatches 13; Indels 3; Gaps 2;

Qy   2 VQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYA 61
         ||||:||||||:|||||||||:|||||| |::|:||||||||||||||| |||:||:| :
Db   1 VQLQESGAELVKPGASVKLSCTTSGFNIQDTYMHWVKQRPEQGLEWIGRIDPANGNTHFD 60

Qy 62 PNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITFAYWGQGTLVTVSA 116
         |:||:|||:|||||||||||||||||||||||||| | || ||:|||||||
Db 61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAG-YYFDVWGQGTTVTVSS 116

RESULT 15
JC5322
p53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match   72.4%; Score 446.5; DB 2; Length 233;
Best Local Similarity 77.7%; Pred. No. 3.2e-34;
Matches 87; Conservative 7; Mismatches 15; Indels 3; Gaps 1;

Qy   5 QQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYAPNF 64
            :||||||:|||||||||||||||:|||.|:|||||||||||||||||||:|||||||.:
Db   1 QESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSS 60

Qy   65 QGRATWTADTSSNTAYLQLSSLTSEDTAVYYCVGGTITPAYWGQGTLVTVSA 116
            |||||||||||||||||||||||||||||||||||| |||||:
Db   61 GVKATWTADTSSNTAYLQLSSLTSEDTAVYYCNAG---MDYWGQGTTVTVSS 109

Search completed: December 29, 2004, 18:06:56
Job time : 16.0782 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: December 29, 2004, 17:37:57 ; Search time 79.7286 Seconds
(without alignments)
521.928 Million cell updates/sec

Title: US-10-774-076-4
Perfect score: 617
Sequence: 1 EVQLQQSGAELVRSGASVKL..........YGGTITFAYWGQGTLVTVSA 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	537	87.0	122	7	ABR61864	Mouse MAb
2	537	87.0	122	7	ADQ31245	Murine 1A
3	528	85.6	122	8	ADQ31285	Humanised
4	526	85.3	243	2	AAW60769	Single ch
5	523	84.8	118	2	AAW01586	Lead bind
6	519	84.1	116	3	AAY70787	Murine an
7	516	83.6	535	2	AAW28491	Human p53
8	516	83.6	535	2	AAW28492	Human p53
9	514.5	83.4	119	6	AAW89635	2A2 monoc
10	511	82.8	112	2	ABB99635	Anti-p53
11	508	82.3	124	2	AAW89173	Anti-carc
12	506	82.0	266	8	AAR60566	Anti-carc
13	505	81.8	120	2	ADH77307	Yeast kil
14	505	81.8	255	2	AAW41387	Anti-CEA
15	505	81.8	281	2	AAW41394	Chimeric
16	505	81.8	642	2	AAW82744	Fusion pr
17	505	81.8	666	2	AAW82741	806.077 h
18	503	81.5	124	2	AAW82745	Fusion pr
19	503	81.5	124	6	AAR60565	Anti-carc
20	503	81.5	124	6	AAR60565	Anti-carc
21	503	81.5	124	6	ABG75594	Mouse mon
22	502	81.4	124	8	ADN08039	mCOL-1 VH
23	502	81.4	120	8	ADK18142	CAB1 heav
24	502	81.4	244	8	ADJ54095	CAB1 hea
25	502	81.4	244	8	ADK18141	CAB1-scFv
26	502	81.4	270	2	AAR75719	MFE-23 an
27	502	81.4	556	4	AAU80040	ScFv-rear
28	502	81.4	556	4	AAU97935	ScFv-rear
29	501	81.2	556	4	AAU76694	Mouse hea
30	501	81.2	136	4	AAB35290	Murine PS
31	501	81.2	553	2	AAW11508	Single ch
32	501	81.2	553	2	AAW73223	H22-anti-
33	501	81.2	553	4	AAB61960	Bispecifi
34	501	81.2	553	4	AAB85455	Bispecifi
35	500	81.0	137	2	AAR95948	HNk-20 va
36	498.5	80.8	254	2	AAY30117	Murine an
37	498.5	80.8	254	2	AAY30119	Murine an
38	498.5	80.8	254	2	AAY30123	Murine an
39	498.5	80.8	254	2	AAY30121	Murine an
40	496	80.4	124	2	AAY39528	Murine CO
41	496	80.4	124	5	AAU76632	Murine Co
42	496	80.4	124	5	AB007328	Murine ca
43	496	80.4	124	6	ABU09037	Murine CO
44	496	80.4	124	8	ADH29099	Mouse mon
45	495.5	80.3	117	4	AAB82709	VEGF anta

ALIGNMENTS

RESULT 1
ABR61864

ID   ABR61864 standard; protein; 122 AA.
XX
AC   ABR61864;
XX
DT   12-SEP-2003 (first entry)
XX
DE   Mouse MAb 1A1 heavy chain variable region sequence.
XX
KW   Antibody; beta-chemokine; monocyte chemotactic protein; MCP-1; MCP-2;
KW   MCP-3; antiinflammatory; nephrotrophic; dermatological; hepatotrophic;
KW   neuroprotective; antiatherosclerotic; antirheumatic; antiarthritic;
KW   cytostatic; anticonvulsant; antidiabetic; ophthalmological; vasotropic;
KW   immunomodulator; cerebroprotective; antiulcer; antiparkinsonian; MAb;
KW   monoclonal antibody; 1A1.
XX
OS   Mus musculus.
XX
XX
PN   WO2003048083-A2.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038229.
XX
PR   30-NOV-2001; 2001US-0343391P.
PR   24-MAY-2002; 2002US-0383277P.
PR   01-AUG-2002; 2002US-0400469P.
XX
PT   Novel antibody or its antigen binding fragment that specifically binds to
PT   monocyte chemotactic protein-2 and other beta-chemokine, useful for
PT   detecting presence of beta-chemokine in sample, and blocking chemotaxis.
XX
PA   (BIOJ) BIOGEN INC.
XX
PI   De Fougerolles AR, Kotelianski VE, Garber E, Reid C;
XX
DR   WPI; 2003-532819/50.
DR   N-PSDB; ACC84729.
XX
PS   Example 8; Page 66; 100pp; English.
XX
CC   The invention relates to an antibody or its antigen binding fragment (AF)
CC   that specifically binds to a plurality of beta-chemokines, particularly
CC   monocyte chemotactic proteins MCP-1, MCP-2 and MCP-3. The antibodies are
CC   useful in an immunoassay method for detecting the presence of a beta-
CC   chemokine in a sample, and for blocking chemotaxis. The antibodies or
CC   their AFs are useful for treating a subject suffering from a disorder

CC chosen from glomerulonephritis, scleroderma, multiple sclerosis, lupus
CC nephritis, cirrhosis, atherosclerosis, inflammatory bowel disease or
CC rheumatoid arthritis. The antibodies are also useful for treating
CC oncogenic disease or cancer, Crohn's disease, diabetic nephropathy,
CC cachexia, stroke, ulcerative colitis, coronary restenosis, Huntington's
CC disease and Parkinson's disease. The present sequence represents a murine
CC monoclonal antibody (MAb) 1A1 heavy chain variable region
XX
SQ Sequence 122 AA;

Query Match   87.0%; Score 537; DB 7; Length 122;
Best Local Similarity   84.8%; Pred. No. 3.8e-41;
Matches 106; Conservative   3; Mismatches   4; Indels 12; Gaps   2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
               |:|||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC------------YGGTITFAYWGQGTTL 111
               |||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   61 APKFQGKATMTADTSSNTAYLQLSSLTSEDTAVYYCNTWAYYGTTSYGG---FAYWGQGTTI 117

Qy   112 VTVSA 116
               |||:|
Db   118 VTVSS 122

RESULT 2
ID ADQ31245
AC ADQ31245 standard; protein; 122 AA.
XX
DT 09-SEP-2004 (first entry)
XX
DE Murine 1A1 heavy chain variable domain antibody protein SeqID 11.
XX
KW murine; 1A1; monocyte chemotactic protein; beta-chemokine family; MCP-3;
KW glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
KW lupus nephritis; atherosclerosis; inflammatory bowel disease;
KW rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
KW immunopathological disorder; antiatteriosclerotic; antiarthritic;
KW antiinflammatory; antirheumatic; cytostatic; dermatological;
KW hepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP.
XX
OS Mus musculus.
XX
PN WO200405O836-A2.
XX
PD 17-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037834.
XX
PR 27-NOV-2002; 2002US-0430007P.
XX
PA (BIOG-) BIOGEN IDEC MA INC.
XX
PI De Fougerolles AR, Kotelianski VE, Garber E, Reid C, Saldanha JW;
PI Van Vlijmen H;
XX
DR WPI; 2004-461110/43.
DR N-PSDB; ADQ31243.
XX
PT New antibodies against monocyte chemotactic proteins (MCP), useful for
PT treating or preventing disorders associated with detrimental MCP
PT activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or
PT atherosclerosis.
XX
PT Example 9; SEQ ID NO 11, 200pp; English.
XX
PS This invention relates to an antibody for treating or preventing
CC disorders associated with detrimental monocyte chemotactic protein (MCP)
CC activity. Specifically, it refers to humanised antibodies that bind to

CC members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3
CC belong) and in particular antibodies that have been modelled on, and
CC modified from, the variable complementarity determining regions (CDRs) of
CC the murine 11K2 and 1A1 immunoglobulin sequences. The present invention
CC describes using these antibodies to treat or prevent diseases and
CC disorders including glomerulonephritis, scleroderma, cirrhosis, multiple
CC sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases,
CC rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer
CC and immunopathological disorders. Accordingly, they can be used in the
CC development of pharmaceutical compositions that exhibit
CC antiatteriosclerotic, antiarthritic, antiinflammatory, antirheumatic,
CC cytostatic, dermatological, hepatotropic, immunomodulator, nephrotropic
CC and neuroprotective activities. This polypeptide sequence is the murine
CC 1A1 heavy chain antibody protein of the invention.
XX
SQ Sequence 122 AA;

Query Match   87.0%; Score 537; DB 8; Length 122;
Best Local Similarity   84.8%; Pred. No. 3.8e-41;
Matches 106; Conservative   3; Mismatches   4; Indels 12; Gaps   2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
               |:|||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC------------YGGTITFAYWGQGTTL 111
               |||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   61 APKFQGKATMTADTSSNTAYLQLSSLTSEDTAVYYCNTWAYYGTTSYGG---FAYWGQGTTI 117

Qy   112 VTVSA 116
               |||:|
Db   118 VTVSS 122

RESULT 3
ID ADQ31285
AC ADQ31285 standard; protein; 122 AA.
XX
DT 09-SEP-2004 (first entry)
XX
DE Humanised murine 1A1 heavy chain antibody protein SeqID 51.
XX
KW 1A1; monocyte chemotactic protein; beta-chemokine family;
KW glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
KW lupus nephritis; atherosclerosis; inflammatory bowel disease;
KW rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
KW immunopathological disorder; antiatteriosclerotic; antiarthritic;
KW antiinflammatory; antirheumatic; cytostatic; dermatological;
KW hepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP;
KW murine; humanised antibody.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO200405O836-A2.
XX
PD 17-JUN-2004.
XX
PF 25-NOV-2003; 2003WO-US037834.
XX
PR 27-NOV-2002; 2002US-0430007P.
XX
PA (BIOG-) BIOGEN IDEC MA INC.
XX
PI De Fougerolles AR, Kotelianski VE, Garber E, Reid C, Saldanha JW;
PI Van Vlijmen H;
XX
DR WPI; 2004-461110/43.
XX
PT New antibodies against monocyte chemotactic proteins (MCP), useful for
PT treating or preventing disorders associated with detrimental MCP

```
PT   activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or
PT   atherosclerosis.
XX
PS   Disclosure; SEQ ID NO 51; 200pp; English.
XX
CC   This invention relates to an antibody for treating or preventing
CC   disorders associated with detrimental monocyte chemotactic protein (MCP)
CC   activity. Specifically, it refers to humanised antibodies that bind to
CC   members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3
CC   belong) and in particular antibodies that have been modelled on, and
CC   modified from, the variable complementarity determining regions (CDRs) of
CC   the murine 11k2 and 1A1 immunoglobulin sequences. The present invention
CC   describes using these antibodies to treat or prevent diseases and
CC   disorders including glomerulonephritis, scleroderma, cirrhosis, multiple
CC   sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases,
CC   rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer
CC   and immunopathological disorders. Accordingly, they can be used in the
CC   development of pharmaceutical compositions that exhibit
CC   antiartheriosclerotic, antiarthritic, antiinflammatory, antirheumatic,
CC   cytostatic, dermatological, hepatotropic, immunomodulator, nephrotropic
CC   and neuroprotective activities. This polypeptide sequence is the
CC   humanised murine 1A1 variable and constant heavy chain antibody protein
CC   of the invention.
XX
SQ   Sequence 122 AA;

Query Match     85.6%;  Score 528;  DB 8;  Length 122;
Best Local Similarity   85.2%;   Pred. No. 2.5e-40;
Matches 104;  Conservative   2;  Mismatches   4;  Indels  12;  Gaps   2;

Qy    1  EVQLQQSGGSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQREEQGLEWIGCIDPENGDTEY  60
         |||||||     |||||||||||||||||||| ::|::|||||:|||||||| |||||||||||
Db    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIGWIDPENGDTEY  60

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----------YGGTIYPFAYWGQGTL  111
         ||:|||:||||||||||||||||||||||||||||           |||||||||||
Db   61  APKFQGKATMTADTSSNTAYLQLSSLTSEDTAVYYCNTWAYYGTSYGG---FAYWGQGTT  117

Qy  112  VT  113
         ||
Db  118  VT  119
```

RESULT 4
AAW60769

```
ID   AAW60769 standard; protein; 243 AA.
XX
AC   AAW60769;
XX
DT   08-SEP-1998  (first entry)
XX
DE   Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
XX
KW   Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;
KW   regulatory domain; p53 mutant; H273; W248; G281;
KW   p53-dependent trans-activating activity; restoration;
KW   tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;
KW   cancer; re-stenosis; ss.
XX
OS   Mus sp.
XX
PN   WO9818825-A1.
XX
PD   07-MAY-1998.
XX
PF   27-OCT-1997;  97WO-FR001921.
XX
PR   29-OCT-1996;  96FR-0001921.
XX
PA   (RHON ) RHONE-POULENC RORER SA.
XX
PI   Bracco L, Debussche L;
XX
```

```
DR   WPI; 1998-272140/24.
DR   N-PSDB; AAV36236.
XX
PT   Restoring p53-dependent trans-activating activity to cell containing
PT   mutant p53 - by delivering single-chain antibody specific for the mutant,
PT   particularly for treatment of tumours.
XX
PS   Claim 5; Page 31; 54pp; French.
XX
CC   The present sequence represents a single chain antibody (ScFv) designated
CC   421. The antibody binds to an epitope present in the C-terminal region of
CC   the p53 protein that includes oligomerisation and regulatory domains,
CC   specifically between positions 320 and 393. ScFv 421 is directed against
CC   p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
CC   introduced into cells containing a mutant p53 protein, p53-dependent
CC   trans-activating activity is restored. ScFv 421 is specific for p53-
CC   mutants that have lost tumour-suppressing activity and are present in
CC   tumour cells. It is particularly used to treat hyper-proliferation
CC   associated with these mutants (e.g. cancer and re-stenosis) but may also
CC   be used in vitro for studying mechanisms of activity of p53 or its mutant
CC   and to purify or detect p53
XX
SQ   Sequence 243 AA;

Query Match     85.3%;  Score 526;  DB 2;  Length 243;
Best Local Similarity   86.4%;   Pred. No. 8.1e-40;
Matches 102;  Conservative   5;  Mismatches   7;  Indels  4;  Gaps   2;

Qy    1  EVQLQQSGGSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQREEQGLEWIGCIDPENGDTEY  60
         |||||||     ||||||||||||||||||||||||:|||||:|||||||| |||||||||||
Db    1  QVQLQQSGAELVRSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY  60

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----------YGGTIYPFAYWGQGTLVTVSA  116
         ||:|||:|||||||||||||||||| |||||||||           |:||||||:
Db   61  APKFQGKATMTADTSSNTAYLQLSSLASEDTAVYYCNFYGDALD--YWGQGTTVTVSS  116
```

RESULT 5
AAW01586

```
ID   AAW01586 standard; protein; 118 AA.
XX
AC   AAW01586;
XX
DT   22-AUG-1997  (first entry)
XX
DE   Lead binding MAb 14G11 heavy chain variable region.
XX
KW   Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW   pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW   heavy metal.
XX
OS   Mus musculus.
XX
PN   WO9639518-A1.
XX
PD   12-DEC-1996.
XX
PF   05-JUN-1996;  96WO-US009258.
XX
PR   05-JUN-1995;  95US-00462798.
PR   10-OCT-1995;  95US-0054173.
XX
PA   (BION-) BIONEBRASKA INC.
XX
PI   Wylie DB, Lopez O, Murray PJ;
XX
DR   WPI; 1997-043140/04.
DR   N-PSDB; AAT58260.
XX
PT   DNA encoding heavy metal binding polypeptide sequences - used for
PT   detecting, removing, adding or neutralising heavy metals, such as lead
PT   cations.
XX
```

Claim 12; Page 75; 125pp; English.

PS
XX
CC The present sequence represents the heavy chain variable region for
CC monoclonal antibody (MAb) 14G11, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the heavy
CC metals in biological and inanimate systems. It can be used in e.g.
CC aqueous liquid systems, in biological or environmental systems or in such
CC compositions as perfumes, cosmetics, pharmaceuticals, health care
CC products, skin treatment products, pesticides, herbicides, solvents used
CC in the production of semi-conductor and integrated circuit components and
CC for applications involving minute amounts of specific heavy metals
CC production materials for electronic components. The products can provide
SQ Sequence 118 AA;

RESULT 6
AAY70787
ID AAY70787 standard; protein; 116 AA.
XX
AC AAY70787;
XX
DT 31-JUL-2000 (first entry)
XX
DE Murine anti-p53 monoclonal antibody PAb-421 heavy chain variable region.
XX
KW Murine; p53 protein; monoclonal antibody; PAb-421; DNA-binding domain;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
KW heavy chain variable region; VH; complementarity determining region; CDR.
OS Mus sp.
XX
FH Key   Location/Qualifiers
FT Region   26..35
FT   /label= CDR
FT   /note= "Complementarity determining region"
FT Region   50..66
FT   /label= CDR
FT   /note= "Complementarity determining region"
FT Region   99..105
FT   /label= CDR
FT   /note= "Complementarity determining region"
XX

Query Match   84.8%; Score 523; DB 2; Length 118;
Best Local Similarity   86.4%; Pred. No. 6.9e-40;
Matches 102; Conservative   3; Mismatches 11; Indels   2; Gaps   1;

Qy   1 EVOLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 EVOLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITFAYWGQGTLVTVSA 116
        ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   61 DPKFQGKATMTADTSSNIAYLQLSSLTSEDTAVYYCNPYGYDDAMDVWGQGTSVTVSS 118

Cohen IR, Rotter V, Brez-Alon N, Herkel J;
(YEDA) YEDA RES & DEV CO LTD.
98US-0148P.
19-OCT-1998;
99WO-US024443.
19-OCT-1999;
WO2002082-A1.
27-APR-2000.
WPI; 2000-335512/29.
Treatment of systemic lupus erythematosus by down-regulating the

RESULT 7
AAW28491
ID AAW28491 standard; protein; 535 AA.
XX
AC AAW28491;
XX
DT 25-NOV-1997 (first entry)
XX
DE Human p53 protein variant 8-325 encoded by pEC176.
XX
KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW tumour suppression; apoptosis; single chain antibody variable domain.
OS Homo sapiens.
OS Herpes simplex virus.
OS Synthetic.
OS Chimeric.
XX
PN WO9704092-A1.
PD 06-FEB-1997.
PF 17-JUL-1996; 96WO-FR001111.
PR 19-JUL-1995; 95FR-0008729.
PA (RHON) RHONE POULENC RORER SA.
PI Conseiller E, Bracco L;
XX
DR WPI; 1997-132633/12.
DR N-PSDB; AAT86221.
XX
PT New p53 variants e.g. with oligomerisation domain replaced by leucine
PT zipper - useful for treating hyper-proliferative disorders, esp. cancer
PT and restenosis.

Claim 36; Page 88-90; 133pp; French.

Claimed variants of protein p53 have at least part of the oligomerisation

CC domain deleted and replaced by a leucine zipper domain. The mutants
CC preferably also have at least part of the p53 transactivation domain
CC (amino acids 1-74) deleted and replaced by the transactivating domain
CC (TD) from herpes simplex virus viral protein VP16 (amino acids 411-490)
CC or by a protein domain able to bind selectively to a transactivator,
CC especially a single-chain antibody variable domain (ScFv). The present
CC sequence is that of a specifically claimed p53 variant designated S-325
CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
CC and a leucine zipper domain at the C-terminal. The p53 variants are more
CC active and more stable tumour suppressors and apoptosis-inducing agents
CC than wild-type p53 and are active where the wild-type protein is not,
CC i.e. they are not inactivated by dominant negative or oncogenic mutants,
CC nor by other cellular proteins (because the leucine zipper domain
CC prevents formation of inactive mixed oligomers)
XX
SQ Sequence 535 AA;

```
Query Match             83.6%;  Score 516;  DB 2;  Length 535;
Best Local Similarity   84.7%;
Matches  100;  Conservative   6;  Mismatches   8;  Indels   4;  Gaps   2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        :||||:||||| |||||||||||||||||||||:|||||||||||||||||  ||||||||
Db   3 QVQLQESGAELVGSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 62

Qy  61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITPAYWGQGTLVTVSA 116
        ||:|||:||||||||||||||||||||:||||||||  :  |  || ||||||:||||:
Db  63 APKFQGKATMTADTSSNTAYLQLSSLASEDTAVYYCNFYGDALD--YWGQGTTVTVSS 118
```

RESULT 8
AAW28492
ID AAW28492 standard; protein; 535 AA.
XX
AC AAW28492;
XX
DT 25-NOV-1997 (first entry)
XX
DE Human p53 protein variant S-325H.
XX
KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW tumour suppression; apoptosis; single chain antibody variable domain.
XX
OS Homo sapiens.
OS Herpes simplex virus.
OS Synthetic.
OS Chimeric.
XX
FH Key   Location/Qualifiers
FT Misc-difference 361
FT   /note= "Arg residue at position 182 of wild-type p53 has
FT   been mutated to His"
XX
PN WO9704092-A1.
XX
PD 06-FEB-1997.
XX
PF 17-JUL-1996; 96WO-PR001111.
XX
PR 19-JUL-1995; 95FR-00008729.
XX
PA (RHON) RHONE POULENC RORER SA.
XX
PI Conseiller B, Bracco L;
XX
DR WPI; 1997-132633/12.
XX
PT New p53 variants e.g. with oligomerisation domain replaced by leucine
PT zipper - useful for treating hyper-proliferative disorders, esp. cancer
PT and restenosis.
XX

PS Claim 36; Page; 133pp; French.
XX
CC Claimed variants of protein p53 have at least part of the oligomerisation
CC domain deleted and replaced by a leucine zipper domain. The mutants
CC preferably also have at least part of the p53 transactivation domain
CC (amino acids 1-74) deleted and replaced by the transactivating domain
CC (TD) from herpes simplex virus viral protein VP16 (amino acids 411-490)
CC or by a protein domain able to bind selectively to a transactivator,
CC especially a single-chain antibody variable domain (ScFv). The present
CC sequence is that of a specifically claimed p53 variant designated S-325H
CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
CC (but with Arg182 replaced by His) and a leucine zipper domain at the C-
CC terminal. The p53 variants are more active and more stable tumour
CC suppressors and apoptosis-inducing agents than wild-type p53 and are
CC active where the wild-type protein is not, i.e. they are not inactivated
CC by dominant negative or oncogenic mutants, nor by other cellular proteins
CC (because the leucine zipper domain prevents formation of inactive mixed
CC oligomers). (Note: this sequence does not appear in the specification and
CC has been produced by modifying the given sequence of variant V-325)
XX
SQ Sequence 535 AA;

```
Query Match             83.6%;  Score 516;  DB 2;  Length 535;
Best Local Similarity   84.7%;
Matches  100;  Conservative   6;  Mismatches   8;  Indels   4;  Gaps   2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
        :||||:||||| |||||||||||||||||||||:|||||||||||||||||  ||||||||
Db   3 QVQLQESGAELVGSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 62

Qy  61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTITPAYWGQGTLVTVSA 116
        ||:|||:||||||||||||||||||||:||||||||  :  |  || ||||||:||||:
Db  63 APKFQGKATMTADTSSNTAYLQLSSLASEDTAVYYCNFYGDALD--YWGQGTTVTVSS 118
```

RESULT 9
ABB99635
ID ABB99635 standard; protein; 119 AA.
XX
AC ABB99635;
XX
DT 28-MAR-2003 (first entry)
XX
DE 2A2 monoclonal antibody heavy chain variable region.
XX
KW Heavy chain; variable region; monoclonal antibody; 2A2; cathepsin B;
KW cancer; arthritis.
XX
OS Mus sp.
XX
PN WO200294881-A2.
XX
PD 28-NOV-2002.
XX
PF 02-APR-2002; 2002WO-SI000013.
XX
PR 18-MAY-2001; 2001SI-00000132.
XX
PA (KRKA) KRKA TOVARNA ZDRAVIL DD.
XX
PI Kos J, Premzl A, Kopitar Jerala N, Fan X, Turk V, Bestagno M;
PI Burrone OR;
XX
DR WPI; 2003-120791/11.
DR N-PSDB; ABV77141.
XX
PT New neutralizing antibodies directed against Cathepsin B, useful for
PT treating and/or diagnosing a disease associated with an increased
PT cathepsin B activity or concentration, e.g. cancer or arthritis.
XX
PS Claim 3; Fig 6; 44pp; English.
XX
CC The present sequence represents the heavy chain variable region of the

Left column

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CC   murine monoclonal antibody 2A2. 2A2 is a neutralizing antibody which is
CC   directed against cathepsin B. The antibody is useful for treating and
CC   diagnosing a disease associated with an increased cathepsin B activity,
CC   such as cancer or arthritis. The antibody is also useful for
CC   manufacturing a medicament for treating or diagnosing these diseases
XX
SQ   Sequence 119 AA;

Query Match            83.4%;
Best Local Similarity  83.2%;
Matches  99;  Conservative   6;  Pred. No. 4.1e-39;
                                  Mismatches  11;  Indels  3;  Gaps  1;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
            : |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  QVQLQQSGAELVRSGASIKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY  60

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYG---GTITFAYWGQGTLVTVSA  116
            |:||||||||||||||||||||||||||||||||      |||||||||||||||:
Db   61  APKFRGRATMTADTSSKTAYLQLSSLTSEDTAVYYCNARRHGIYEMDYWGQGTSVTVSS  119
```

```
RESULT 10
ID   AAW89173 standard; peptide; 112 AA.
XX
AC   AAW89173;
XX
DT   25-MAR-1999  (first entry)
XX
DE   Anti-p53 monoclonal antibody 421 variable heavy chain sequence.
XX
KW   Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW   immune response; tumour associated antigen; metastatic cancer.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO9856416-A1.
XX
PD   17-DEC-1998.
XX
PF   09-JUN-1998;   98WO-IL000266.
XX
PR   09-JUN-1997;   97IL-0121041.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Cohen IR, Rotter V, Wolkowicz R, Ruiz PJ, Erez-Alon N, Herkel J;
XX
DR   WPI; 1999-070296/06.
XX
PT   Use of a monoclonal antibody to a tumour-associated antigen - to induce
PT   anti-tumour immunity or elicit an increased immune response to the
PT   antigen.
XX
CC   Example 3; Fig 3; 47pp; English.

The present invention describes the use of an immunogen (A) to induce
anti-tumour immunity; to elicit an increased immune response to tumour
associated antigen (TAA) and/or to induce an immune response to mutant or
wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
(MAb) to TAA, or its fragment; (ii) on the heavy or light chain of MAb
(complementarity determining region) able to elicit antibodies to TAA; or
(iii) a DNA that encodes the variable (V) region of MAb, in a gene delivery vehicle. The present
sequence represents the variable heavy chain sequence from anti-p53 MAb
421. Also described is a method for generating sequence-specific, anti-
DNA antibodies (Ab) by immunising a mammal with a MAb directed to a
domain containing a DNA-binding site of a DNA-binding protein. (A) is
used to treat a wide variety of primary and metastatic cancers,
particularly those where p53 is involved. Ab are used for diagnosis (e.g
to determine critical sequences in animal or plant breeding); to identify
bacteria and other parasites; to determine parentage; in forensic science
```

Right column

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CC   ; to isolate specific genes for DNA vaccination; in gene sequencing and
CC   cloning; also possibly for activation of selected therapeutic genes in
CC   plants, animals and humans. (A) induce an effective anti-tumour response
CC   without causing harm to the patient. The method uses (A) to generate anti
CC   -TAA by exploiting the anti-idiotype network
XX
SQ   Sequence 112 AA;

Query Match            82.8%;
Best Local Similarity  86.8%;
Matches  99;  Conservative   4;  Pred. No. 8e-39;
                                  Mismatches  7;  Indels  4;  Gaps  2;

Qy    4  LQQSGGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYAPN  63
            |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  LQESGAELVRSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEYAPK  60

Qy   64  FQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC---YGGTITFAYWGQGTLVTVS  115
            ||||||||||||||||||||||||||||||||      ||||||||||||||||
Db   61  FQGRATMTADTSSNTAYLQLSSLASEDTAVYYCNFYGDALD--YWGQGTTVTVS  112
```

```
RESULT 11
ID   AAR60566 standard; protein; 124 AA.
XX
AC   AAR60566;
XX
DT   16-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   25-APR-1995  (first entry)
XX
DE   Anti-carcinoembryonic antigen chimeric heavy chain Ab.
XX
KW   Anti-carcinoembryonic antigen chimeric antibodies; CEAS;
KW   chimeric human-murine; breast or colorectal carcinoma; heavy chain.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO9419466-A2.
XX
PD   01-SEP-1994.
XX
PF   16-FEB-1994;   94WO-US001709.
XX
PR   16-FEB-1993;   93US-00017570.
XX
PA   (DOWC ) DOW CHEM CO.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Gourlie BB, Rixon MW, Mezes PS, Kaplan DA, Schlom J;
XX
DR   WPI; 1994-294331/36.
DR   N-PSDB; AAQ71396.
XX
PT   Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis and
PT   therapy of carcinoma, e.g. breast or colorectal carcinoma.
XX
CC   Claim 14; Page 53; 67pp; English.

AAQ71396 codes for AAR60566 the antibody heavy chain region of murine-
human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be
used in in vitro immunoassays for the detection of CEA, and monitoring of
tumour-associated antigen during therapy. It can also be used in vivo
diagnostically, or in therapy for the treatment of tumours associated
with colorectal and breast carcinoma, as well those of the
gastrointestinal tract, lung, ovary and pancreas. (Updated on 25-MAR-2003
to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 124 AA;

Query Match            82.3%;  Score 508;  DB 2;  Length 124;
```

Best Local Similarity   81.5%; Pred. No. 1.7e-38;
Matches 101; Conservative   4; Mismatches 11; Indels   8; Gaps   2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
            |||||||||||||||||||||||||||||||::|||||||||||||||||||||||||||
Db   1 EVQLQQSGAELVRSGASVKMSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 60

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTIT----FAYWGQGTLV 112
            ||||||:||||||||||||||||||||||||||||| |||||| ||||||||||
Db   61 APKFQGKATMTDTSSNTAYLQLSSLTSEDTAVYYCNRGLSTMITTRWFPDVWGAGTTV 120

Qy   113 TVSA 116
            ||:
Db   121 TVSS 124

RESULT 12
ADH77307
ID   ADH77307 standard; protein; 266 AA.
XX
AC   ADH77307;
XX
DT   15-APR-2004 (first entry)
XX
DE   Yeast killer toxin related anti-idiotypic scFv (H20).
XX
OS   Unidentified.
XX
KW   variable region; anti-idiotypic antibody; yeast killer toxin;
KW   microbial infection; viral infection; candidosis; aspergillosis;
KW   cryptococcosis; sporotrychosis; blastomycosis; histoplasmosis; thrush;
KW   tuberculosis; mycobacteriosis; respiratory infection; scarlet fever;
KW   pneumonia; impetigo; rheumatic fever; sepsis; septicaemia;
KW   cutaneous leishmaniasis; visceral leishmaniasis; keratitis;
KW   cystic fibrosis; typhoid fever; gastroenteritis; flu; influenza; HIV;
KW   AIDS; H20.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 126
FT   /note= "Encoded by TTC"
XX
PN   WO20020309493-A2.
XX
PD   20-NOV-2003.
XX
PF   09-MAY-2003; 2003WO-IB002348.
XX
PR   10-MAY-2002; 2002GB-0010783.
XX
PA   (UYSI-) UNIV SIENA.
PA   (POLO/) POLONELLI L.
PA   (CASS/) CASSONE A.
XX
PI   Polonelli L, Cassone A;
XX
PA   Polonelli L, Cassone A;
XX
DR   WPI; 2004-012091/01.
DR   N-PSDB; ADH77306.
XX

PT   New toxin-related polypeptides comprising a fragment of a variable region
PT   of an anti-idiotypic antibody which recognizes the idiotope of an
PT   antibody specific for a yeast killer toxin, useful for treating microbial
PT   or viral infections.
XX
PS   Disclosure; SEQ ID NO 22; 70pp; English.

The invention comprises a polypeptide which contains a part of the
variable region of an anti-idiotypic antibody which recognizes the
idiotope of an antibody specific for a yeast killer toxin. The
polypeptide of the invention is useful for the treatment of microbial and
viral infections, such as: candidosis, aspergillosis, cryptococcosis,
sporotrychosis, blastomycosis, histoplasmosis, thrush, tuberculosis,
mycobacteriosis, respiratory infections, scarlet fever, pneumonia,
impetigo, rheumatic fever, sepsis, septicaemia, cutaneous and visceral

CC   leishmaniasis, keratitis, cystic fibrosis, typhoid fever, gastroenteritis
CC   and haemolytic-uremic syndrome, flu, influenza or HIV/AIDS. The present
CC   amino acid sequence represents an anti-idiotypic antibody (H20) of the
CC   invention.
XX
SQ   Sequence 266 AA;

Query Match   82.0%; Score 506; DB 8; Length 266;
Best Local Similarity   77.8%; Pred. No. 5.9e-38;
Matches 98; Conservative   7; Mismatches 11; Indels 10; Gaps   2;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
            |||||||||:|||||||||||||||||||||||:||||||||||||||||||:||||||
Db   3 QVQLQQSGAKLVRSGASVKLSCTTSGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEY 62

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC------YGGTITP---AYWGQGT 110
            ||::||:|:||||||||||||||||||||||||||| ||||||| ||||||||
Db   63 APKFQGKTTLTADTSSNTAYLQLSSLTSEDTAVYYCNAWVDGYSGDFYYYAMDYWGQGT 122

Qy   111 LVTVSA 116
            ||:||:
Db   123 TVTCSS 128

RESULT 13
AAW41387
ID   AAW41387 standard; protein; 120 AA.
XX
AC   AAW41387;
XX
DT   02-JUN-1998 (first entry)
XX
DE   Anti-CEA antibody 806.077 heavy chain variable region.
XX
OS   Synthetic.
XX
KW   Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW   cancer diagnosis; complementarity determining region; heavy chain.
XX
PN   WO9742329-A1.
XX
PD   13-NOV-1997.
XX
PF   29-APR-1997; 97WO-GB001165.
XX
PR   04-MAY-1996; 96GB-00009405.
PR   14-FEB-1997; 97GB-00003103.
XX
PA   (ZENE) ZENECA LTD.
XX
PI   Copley CG, Edge MD, Emery SC;
XX
DR   WPI; 1997-589987/51.
DR   N-PSDB; AAV17269.
XX
PT   Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis
PT   and therapy of cancer.
XX
PS   Claim 3; Page 196; 208pp; English.

This sequence is the heavy chain variable region of the antibody of the
invention. The antibody is an anti-CEA (carcinoembryonic antigen)
antibody (806.077 Ab). Host cells or transgenic organisms transformed
with DNA encoding the antibody, are used to make the antibody or
conjugate. The conjugate is used in a medicament suitable for intravenous
administration. The conjugate can be used for cancer therapy, selectively
killing tumour cells. The antibody can be used for in vivo or in vitro
diagnosis of cancer.
XX
SQ   Sequence 120 AA;

Query Match   81.8%; Score 505; DB 2; Length 120;
Best Local Similarity   80.8%; Pred. No. 3e-38;

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Qy          Matches  97; Conservative    7; Mismatches   12; Indels    4; Gaps    1;

RESULT 14
AAW41394
ID   AAW41394 standard; protein; 255 AA.
XX
AC   AAW41394;
XX
DT   17-OCT-2003  (revised)
DT   02-JUN-1998  (first entry)
XX
DE   Chimeric anti-CEA antibody 806.077 HuIgG2 Fd chain.
XX
KW   Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW   cancer diagnosis; complementarity determining region; Fd chain.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
XX
PN   WO9742329-A1.
XX
PD   13-NOV-1997.
XX
PF   29-APR-1997;  97WO-GB001165.
XX
PR   04-MAY-1996;  96GB-00009405.
PR   14-FEB-1997;  97GB-0000103.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Copley CG,  Edge MD,  Emery SC;
XX
DR   WPI; 1997-558987/51.
DR   N-PSDB; AAV17291.
XX
PT   Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis
PT   and therapy of cancer.
XX
PS   Example 8; Page 102-103; 208pp; English.
XX
CC   This sequence is the HuIgG2 Fd chain region of the antibody of the
CC   invention. The antibody is an anti-CEA (carcinoembryonic antigen)
CC   antibody (806.077 Ab). Host cells or transgenic organisms transformed
CC   with DNA encoding the antibody, are used to make the antibody or
CC   conjugate. The conjugate is used in a medicament suitable for intravenous
CC   administration. The conjugate can be used for cancer therapy, selectively
CC   killing tumour cells. The antibody can be used for in vivo or in vitro
CC   diagnosis of cancer. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 255 AA;

Qy          1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
               |||||||||||||||||||||||||||||||:||:|||||||||||||||||||||||
Db          1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDTEY 60

Qy         61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVSA 116
               |:||:|||||||||||||||||||||||||||||       ||||||||||||||||:
Db         61 APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 120
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Qy          Matches  97; Conservative    7; Mismatches   12; Indels    4; Gaps    1;
Best Local Similarity   80.8%;  Pred. No. 7e-38;
Matches  97; Conservative    7; Mismatches   12; Indels    4; Gaps    1;

Query Match         81.8%;  Score 505;  DB 2;  Length 255;

Qy          1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
               |||||||||||||||||||||||||||||||:||:|||||||||||||||||||||||
Db         20 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDTEY 79

Qy         61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVSA 116
               |:||:|||||||||||||||||||||||||||||       ||||||||||||||||:
Db         80 APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 139
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RESULT 15
AAW82744
ID   AAW82744 standard; protein; 281 AA.
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AC   AAW82744;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Fusion protein pICI266/806IscFvtag/his.
XX
KW   Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
KW   prodrug-converting enzyme; cell surface antigen; treatment; cancer;
KW   inflammation; rheumatoid arthritis; antibody; prodrug therapy system.
XX
OS   Synthetic.
XX
PN   WO9851787-A2.
XX
PD   19-NOV-1998.
XX
PF   05-MAY-1998;  98WO-GB001294.
XX
PR   10-MAY-1997;  97GB-00009421.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Emery SC,  Blakey DC;
XX
DR   WPI; 1999-059700/05.
DR   N-PSDB; AAV72069.
XX
PS   Example 16; Page 84-85; 100pp; English.
XX
CC   This sequence is a used in a method for obtaining a novel gene construct
CC   (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-
CC   targeting group (I) and a heterologous prodrug-converting enzyme (II),
CC   and (B) is directed to leave the cell for selective localisation at a
CC   cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target
CC   site, then administration of (III) is used for targeted release of
CC   cytotoxic drug, specifically for treating cancer but also inflammation
CC   such as rheumatoid arthritis. In situ generation of the targeting
CC   antibody increases selectivity, reducing side effects at normal tissue.
CC   The method is applicable to any antibody-directed enzyme prodrug therapy
CC   system
XX
SQ   Sequence 281 AA;

Qy          Matches  97; Conservative    7; Mismatches   12; Indels    4; Gaps    1;
Best Local Similarity   80.8%;  Pred. No. 7.8e-38;
Matches  97; Conservative    7; Mismatches   12; Indels    4; Gaps    1;

Query Match         81.8%;  Score 505;  DB 2;  Length 281;

Qy          1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
               |||||||||||||||||||||||||||||||:||:|||||||||||||||||||||||
Db         23 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDTEY 82

Qy         61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC-----YGGTITFAYWGQGTLVTVSA 116
               |:||:|||||||||||||||||||||||||||||       ||||||||||||||||:
Db         83 APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 142
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Search completed: December 29, 2004, 17:57:29
Job time : 82.7286 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on:　　　December 29, 2004, 18:05:34 ; Search time 67.0678 Seconds
　　　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　　　622.182 Million cell updates/sec

Title:　　　　　US-10-774-076-4
Perfect score:　617
Sequence:　　　1 EVQLQQSGAELVRSGASVKL..........YGGTITFAYWGQGTLVTVSA 116

Scoring table:　BLOSUM62
　　　　　　　Gapop 10.0 , Gapext 0.5

Searched:　　　1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters:　1599051

Post-processing: Minimum Match 0%
　　　　　　　Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :　Published Applications AA:*
　　　　　1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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　　　　　3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
　　　　　4: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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　　　　　6: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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　　　　　8: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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　　　　14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
　　　　15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
　　　　16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
　　　　17: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
　　　　18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
　　　　19: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
　　　　20: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

SUMMARIES

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1	617	100.0	116	17	US-10-774-076-4	Sequence 4, Appli
2	516	83.6	535	9	US-09-968-851-38	Sequence 38, Appl
3	511	82.8	112	13	US-10-032-482-7	Sequence 7, Appli
4	507	82.2	136	9	US-09-564-329A-11	Sequence 11, Appl
5	507	82.2	136	9	US-09-885-153-11	Sequence 11, Appl
6	507	82.2	136	9	US-09-854-811-11	Sequence 11, Appl
7	507	82.2	136	9	US-09-934-773-11	Sequence 11, Appl
8	507	82.2	136	9	US-09-963-620-11	Sequence 11, Appl
9	507	82.2	136	10	US-09-855-632-11	Sequence 11, Appl
10	507	82.2	136	14	US-10-225-784-11	Sequence 11, Appl
11	507	82.2	136	14	US-10-225-720-11	Sequence 11, Appl
12	507	82.2	136	14	US-10-225-779-11	Sequence 11, Appl
13	507	82.2	136	14	US-10-374-381-11	Sequence 11, Appl
14	507	82.2	505	9	US-10-774-076-4	Sequence 4, Appli
15	505	81.8	120	9	US-09-910-059-11	Sequence 11, Appl
16	505	81.8	255	9	US-09-910-059-19	Sequence 19, Appl
17	502	81.4	556	10	US-09-819-266-28	Sequence 28, Appl
18	496	80.4	124	9	US-09-025-403A-1	Sequence 1, Appli
19	496	80.4	124	9	US-09-974-052-1	Sequence 1, Appli
20	496	80.4	124	9	US-09-974-051-1	Sequence 1, Appli
21	496	80.4	124	10	US-09-974-498-1	Sequence 1, Appli
22	496	80.4	124	10	US-09-974-516-1	Sequence 1, Appli
23	495.5	80.3	124	9	US-09-787-787-23	Sequence 23, Appl
24	495.5	80.3	117	9	US-09-798-689-7	Sequence 7, Appli
25	495.5	80.3	117	10	US-09-976-787-22	Sequence 22, Appl
26	495.5	80.3	117	17	US-10-203-399B-7	Sequence 7, Appli
27	495.5	80.3	117	17	US-10-778-910-22	Sequence 22, Appl
28	495.5	80.3	119	8	US-08-996-140-11	Sequence 11, Appl
29	495.5	80.3	238	9	US-09-865-787-29	Sequence 29, Appl
30	495.5	80.3	238	9	US-09-865-198-28	Sequence 28, Appl
31	495.5	80.3	238	10	US-09-798-689-21	Sequence 21, Appl
32	495.5	80.3	238	17	US-10-482-630-28	Sequence 28, Appl
33	495.5	80.3	238	17	US-10-778-910-28	Sequence 28, Appl
34	495.5	80.3	238	8	US-10-778-910-23	Sequence 23, Appl
35	495.5	80.3	248	8	US-08-996-140-23	Sequence 23, Appl
36	495	80.2	241	15	US-10-062-188-8	Sequence 8, Appli
37	495	80.2	241	15	US-10-062-188-5	Sequence 5, Appli
38	491.5	79.7	117	9	US-09-976-787-7	Sequence 7, Appli
39	491.5	79.7	117	9	US-09-865-198-7	Sequence 7, Appli
40	491.5	79.7	117	17	US-10-482-630-7	Sequence 7, Appli
41	491.5	79.7	117	17	US-10-778-910-7	Sequence 7, Appli
42	491.5	79.7	240	9	US-09-976-787-28	Sequence 28, Appl
43	491.5	79.7	240	15	US-09-865-198-27	Sequence 27, Appl
44	491.5	79.7	240	17	US-10-482-630-27	Sequence 27, Appl
45	491.5	79.7	240	17	US-10-778-910-27	Sequence 27, Appl

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-774-076-4

; Sequence 4, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
;　APPLICANT: Protein Design Labs, Inc.
;　APPLICANT: Landolfi, et al.
;　TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
;　TITLE OF INVENTION: Psoriasis
;　FILE REFERENCE: 05882.0064.NPUS01
;　CURRENT APPLICATION NUMBER: US/10/774,076
;　CURRENT FILING DATE: 2004-02-06
;　NUMBER OF SEQ ID NOS: 39
;　SOFTWARE: Patentin version 3.2
;　SEQ ID NO 4
;　LENGTH: 116
;　TYPE: PRT
;　ORGANISM: mus sp.
US-10-774-076-4

　Query Match　　　　　100.0%;　Score 617;　DB 17;　Length 116;
　Best Local Similarity　100.0%;　Pred. No. 2.2e-48;
　Matches 116;　Conservative 0;　Mismatches 0;　Indels 0;　Gaps 0;

Qy　　1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
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Db　　1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60

Qy　61 APNFQGRATMTADTSSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
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Db　61 APNFQGRATMTADTSSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116

RESULT 2
US-09-968-851-38
; Sequence 38, Application US/0968851

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Publication No. US20020193561A1
GENERAL INFORMATION:
  APPLICANT: CONSEILLER, EMMANUEL
  APPLICANT: BRACCO, LAURENT
  TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
    USES THEREOF
  NUMBER OF SEQUENCES: 59
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
      DUNNER, LLP
    STREET: 1300 I Street, NW
    CITY: Washington
    STATE: DC
    COUNTRY: USA
    ZIP: 20005-3315
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/968,851
    FILING DATE: 03-Oct-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/983,035
    FILING DATE: 20-Feb-1998
    APPLICATION NUMBER: PCT/FR96/01111
    FILING DATE: 17-JUL-1996
    APPLICATION NUMBER: FR 95/08729
    FILING DATE: 19-JUL-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Strauss, William L.
    REGISTRATION NUMBER: 47,114
    REFERENCE/DOCKET NUMBER: 03804.0142
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202-408-4000
    TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 535 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-968-851-38

Query Match     83.6%;  Score 516;  DB 9;  Length 535;
Best Local Similarity   84.7%;  Pred. No. 1.6e-38;
Matches  100;  Conservative    6;  Mismatches    8;  Indels    4;  Gaps   2;

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Qy  61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTIFPAYWGQGTLVTVSA  116
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RESULT 3
US-10-032-482-7
Sequence 7, Application US/10032482
Publication No. US20020197270A1

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GENERAL INFORMATION:
  APPLICANT: Cohen, Irun
  APPLICANT: ROTTER, Varda
  APPLICANT: Wolkowicz, Roland
  APPLICANT: RUIZ, Pedro
  APPLICANT: EREZ-ALON, Neta
  APPLICANT: HERKEL, Johannes
  TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
  TITLE OF INVENTION: IMMUNITY
```

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  FILE REFERENCE: COHEN42
  CURRENT APPLICATION NUMBER: US/10/032,482
  CURRENT FILING DATE: 2002-01-02
  PRIOR APPLICATION NUMBER: US/10/032,482
  PRIOR FILING DATE: 2002-01-02
  PRIOR APPLICATION NUMBER: US/09/445,602
  PRIOR FILING DATE: 2001-01-24
  PRIOR APPLICATION NUMBER: PCT/IL98/00266
  PRIOR FILING DATE: 1999-12-09
  PRIOR APPLICATION NUMBER: IL 121041
  PRIOR FILING DATE: 1997-06-09
  NUMBER OF SEQ ID NOS: 25
  SOFTWARE: PatentIn version 3.0
  SEQ ID NO 7:
    LENGTH: 112
    TYPE: PRT
    ORGANISM: Mus musculus
US-10-032-482-7

Query Match     82.8%;  Score 511;  DB 13;  Length 112;
Best Local Similarity   86.8%;  Pred. No. 8.8e-39;
Matches   99;  Conservative    4;  Mismatches    7;  Indels    4;  Gaps   2;

Qy   4  LQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEYAPN  63
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Db   1  LQESGAELVRSGASVKLSCTASGFNIKDYYMHWVKQRPEQGLEWIGWIDPENGDTEYAPK  60

Qy  64  FQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC--YGGTIFPAYWGQGTLVTVS  115
        |||:||||||||||||||||||||:|||||||    ||||||||||||:||||
Db  61  FQGKATMTADTSSNTAYLQLSSLASEDTAVYYCNFYGDALD--YWGQGTTVTVS  112
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RESULT 4
US-09-564-329A-11
Sequence 11, Application US/09564329A
Patent No. US20010055751A1

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GENERAL INFORMATION:
  APPLICANT: Reiter, Robert E.
  APPLICANT: Witte, Owen N.
  APPLICANT: Saffran, Douglas C.
  TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
  FILE REFERENCE: 30435.54US14
  CURRENT APPLICATION NUMBER: US/09/564,329A
  CURRENT FILING DATE: 2000-05-03
  PRIOR APPLICATION NUMBER: 08/814,279
  PRIOR FILING DATE: 1997-03-10
  PRIOR APPLICATION NUMBER: 09/359,326
  PRIOR FILING DATE: 1999-07-20
  PRIOR APPLICATION NUMBER: US/09/564,329A
  PRIOR FILING DATE: 2000-05-03
  PRIOR APPLICATION NUMBER: 09/203,939
  PRIOR FILING DATE: 1998-12-02
  PRIOR APPLICATION NUMBER: 09/038,261
  PRIOR FILING DATE: 1998-03-10
  PRIOR APPLICATION NUMBER: 60/124,658
  PRIOR FILING DATE: 1999-03-16
  PRIOR APPLICATION NUMBER: 60/120,536
  PRIOR FILING DATE: 1999-02-17
  PRIOR APPLICATION NUMBER: 60/113,230
  PRIOR FILING DATE: 1998-12-21
  PRIOR APPLICATION NUMBER: 60/074,675
  PRIOR FILING DATE: 1998-02-13
  PRIOR APPLICATION NUMBER: 60/071,141
  PRIOR FILING DATE: 1998-01-12
  PRIOR APPLICATION NUMBER: 09/251,835
  PRIOR FILING DATE: 1999-02-17
  PRIOR APPLICATION NUMBER: 09/308,503
  PRIOR FILING DATE: 1999-05-25
  NUMBER OF SEQ ID NOS: 27
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 11
    LENGTH: 136
    TYPE: PRT
    ORGANISM: SCID Mice
US-09-564-329A-11

Query Match     82.2%;  Score 507;  DB 9;  Length 136;
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RESULT 5
US-09-855-153-11
Sequence 11, Application US/09855153
Patent No. US20020102666A1
GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 09/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-11

Query Match   82.2%; Score 507; DB 9; Length 136;
Best Local Similarity   84.5%; Pred. No. 2.5e-38;
Matches   98; Conservative   4; Mismatches   10; Indels   4; Gaps   1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
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Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITPAYWGQGTLVTVSA 116
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Db   74 VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA 125

RESULT 6
US-09-854-811-11
; Sequence 11, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 09/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-854-811-11

Query Match   82.2%; Score 507; DB 9; Length 136;
Best Local Similarity   84.5%; Pred. No. 2.5e-38;
Matches   98; Conservative   4; Mismatches   10; Indels   4; Gaps   1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
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Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITPAYWGQGTLVTVSA 116
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Db   74 VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA 125

RESULT 7
US-09-934-773-11
; Sequence 11, Application US/09934773
; Patent No. US20020136689A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/934,773.
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 09/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136

Query Match   82.2%; Score 507; DB 9; Length 136;
Best Local Similarity   84.5%; Pred. No. 2.5e-38;
Matches   98; Conservative   4; Mismatches   10; Indels   4; Gaps   1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||:
Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITPAYWGQGTLVTVSA 116
          ||:|||||||||||||||||||||||||||||||||||||| |||||
Db   74 VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA 125

; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-11

Qy   Query Match   82.2%; Score 507; DB 9; Length 136;
     Best Local Similarity 84.5%; Pred. No. 2.5e-38;
     Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
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Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
         |||:||||||||||||||||||||||||||||||||||| |||||||||||
Db   74 VPKFQGKAITMTADIFSNTAYLHLSSLTSEDTAVYYCKTG---GFWGQGTLLVTVSA 125

RESULT 8
US-09-963-620-11
; Sequence 11, Application US/09963620
; Patent No. US2002014194lA1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-963-620-11

Qy   Query Match   82.2%; Score 507; DB 9; Length 136;
     Best Local Similarity 84.5%; Pred. No. 2.5e-38;
     Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

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         ||||||||||||||||||||||||||||||||:||||:||||||||||||:||||||:
Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
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Db   74 VPKFQGKAITMTADIFSNTAYLHLSSLTSEDTAVYYCKTG---GFWGQGTLLVTVSA 125

RESULT 9
US-09-855-632-11
; Sequence 11, Application US/09855632
; Publication No. US20030113818A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,632
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-632-11

Qy   Query Match   82.2%; Score 507; DB 10; Length 136;
     Best Local Similarity 84.5%; Pred. No. 2.5e-38;
     Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
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Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
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Db   74 VPKFQGKAITMTADIFSNTAYLHLSSLTSEDTAVYYCKTG---GFWGQGTLLVTVSA 125

RESULT 10
US-10-225-784-11
; Sequence 11, Application US/10225784
; Publication No. US20030113820A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,784
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 2000-05-03

; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-784-11.

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Query Match       82.2%;   Score 507;   DB 14;   Length 136;
Best Local Similarity   84.5%;   Pred. No. 2.5e-38;
Matches  98;   Conservative  4;   Mismatches  10;   Indels  4;   Gaps  1;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
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Db   14  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF  73

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA  116
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Db   74  VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA  125
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RESULT 11
US-10-224-720-11
Sequence 11, Application US/10224720
; Publication No. US20030147806A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/224,720
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US/09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-11

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Query Match       82.2%;   Score 507;   DB 14;   Length 136;
Best Local Similarity   84.5%;   Pred. No. 2.5e-38;
Matches  98;   Conservative  4;   Mismatches  10;   Indels  4;   Gaps  1;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
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Db   14  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF  73

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA  116
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Db   74  VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA  125
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RESULT 12
US-10-225-779-11
Sequence 11, Application US/10225779
; Publication No. US20030153016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-779-11

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Query Match       82.2%;   Score 507;   DB 14;   Length 136;
Best Local Similarity   84.5%;   Pred. No. 2.5e-38;
Matches  98;   Conservative  4;   Mismatches  10;   Indels  4;   Gaps  1;

Qy    1  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY  60
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Db   14  EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF  73

Qy   61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA  116
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Db   74  VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA  125
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RESULT 13
US-10-374-381-11
Sequence 11, Application US/10374381
Publication No. US20030228318A1
GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/374,381
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/564,329A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-374-381-11

Query Match   82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||:
Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
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Db   74 VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA 125

RESULT 14
US-10-446-542-11
Sequence 11, Application US/10446542
Publication No. US20040018571A1
GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/446,542
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/855,153
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/038,261
; PRIOR FILING DATE: 1998-03-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-446-542-11

Query Match   82.2%; Score 507; DB 15; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||:
Db   14 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVNQRPDQGLEWIGWIDPENGDTEF 73

Qy   61 APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYCYGGTITFAYWGQGTLVTVSA 116
          ||:||||||||||||||||||||||||||||||||||| ||||||||||||
Db   74 VPKFQGKATMTADIFSNTAYLHLSSLTSEDTAVYYCKTG----GFWGQGTLVTVSA 125

RESULT 15
US-09-910-059-11
Sequence 11, Application US/09910059
Patent No. US20020142359A1
GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 11
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-11

Query Match   81.8%; Score 505; DB 9; Length 120;
Best Local Similarity 80.8%; Pred. No. 3.3e-38;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

Qy   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDYYIHWVKQRPEQGLEWIGCIDPENGDTEY 60
          |||||||||||||||||||||||||||||||||:||||||||||||||||:|||||||||:
Db   1 EVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDTEY 60

```
Qy     61  APNFQGRATMTADTSSNTAYLQLSSLTSEDTAVYYC----YGGTIFFAYWGQGTLVTVSA 116
           || |:||:|||||||||| |||:|||||||||||          ||||||:|||| ||:
Db     61  APKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMDYWGQGTSVAVSS 120
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Search completed: December 29, 2004, 18:41:59
Job time : 69.0678 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 17:37:57 ; Search time 73.5428 Seconds
(without alignments)
521.928 Million cell updates/sec

Title: US-10-774-076-3
Perfect Score: 563
Sequence: 1 DIKMTQSPSSMYASLGERVT.........CLQYDEFYTFGGGTKLEIK 107
Scoring table: BLOSUM62
Scoring table: Gapop 10.0 , Gapext 0.5
Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	556	98.8	107	8	ADE85729	Human Eph
2	556	98.8	107	8	ADL23067	Human Eph
3	554	98.4	237	7	ADE57549	Human Pro
4	554	98.4	237	7	ADD47098	Human Pro
5	554	98.4	237	7	ADD48668	Human Pro
6	551	97.9	355	2	AAW35125	R. pipien
7	551	97.9	358	2	AAW35129	R. pipien
8	551	97.9	355	2	Aaw35129	R. pipien
9	551	97.9	358	2	AAW35127	R. pipien
10	551	97.9	360	2	AAW35130	R. pipien
11	551	97.9	379	2	AAW35128	R. pipien
12	548	97.3	214	2	AAW35126	R. pipien
13	546	97.0	127	2	AAW27089	Mouse mon
14	546	97.0	246	4	AAR95946	HNK-20 va
15	541	96.1	107	4	AAB86037	Murine an
16	541	96.1	107	8	AAW58505	H65 prote
17	541	96.1	129	2	ADI01167	Murine mo
18	534	94.8	107	6	Aar30880	pXOM2. 3/
19	534	94.8	107	7	ABG74702	Murine Mu
20	531.5	94.4	215	2	ABR83156	Mu007 ant
21	531	94.3	107	2	AAR53803	FAB light
22	531	94.0	106	2	AAW23956	Mus muscu
23	529	93.6	107	2	AAW65052	Human L c
24	527	93.6	107	5	AAR92083	Murine 13
25	525	93.3	216	2	ABG31430	Amino aci

26	525	93.3	228	2	AAR14704	V1-Lab-Vh
27	525	93.3	228	2	AAR14789	V1-Lab-Vh
28	525	93.3	235	2	AAR14694	V1-Lab-Vh
29	525	93.3	236	2	AAR14702	Vh-Lab-V1
30	525	93.3	236	2	AAR14703	Vh-Lab-V1
31	525	93.3	236	2	AAR14699	Vh-Lab-V1
32	525	93.3	236	2	AAR14700	Vh-Lab-V1
33	525	93.3	236	2	AAR14701	Vh-Lab-V1
34	523	92.9	104	2	AAR79154	Human IgB
35	523	92.7	142	2	AAR98410	3H1 light
36	522	92.7	142	2	AAR99686	Monoclona
37	522	92.7	142	2	AAE04727	Mouse ant
38	522	92.7	142	2	AAW26728	Anti-idio
39	522	92.7	142	2	AAY49961	Murine MA
40	522	92.7	142	2	AAO14016	Mouse 3H1
41	522	92.7	142	5	ABB08119	Antibody
42	522	92.7	142	6	AAO16294	Mouse 3H1
43	522	92.7	142	7	ADC16715	Light cha
44	519.5	92.3	129	2	AAW09815	PelB-Vr34
45	519.5	92.3	258	2	AAW09820	VL3418-1i

ALIGNMENTS

RESULT 1
ADE85729
ID ADE85729 standard; protein; 107 AA.
XX
AC ADE85729;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human Epha2 antibody EA2 VL chain protein SEQ ID NO:33.
XX
KW cancer; hyperproliferative cell disease; EphA2 antibody;
KW EphA2 agonistic antibody; cytostatic; antiasthmatic; antipsoriatic;
KW antiinflammatory; vasotropic; respiratory; gene therapy;
KW metastatic cancer; asthma; psoriasis; inflammatory bowel disease;
KW smooth muscle restenosis; endothelial restenosis; Crohn's disease;
KW chronic obstructive pulmonary disease; human.
XX
OS Homo sapiens.
XX
PN WO2003094859-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-US015044.
XX
PR 10-MAY-2002; 2002US-0379322P.
PR 14-OCT-2002; 2002US-0418213P.
PR 03-APR-2003; 2003US-0460507P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Kinch MS, Carles-Kinch K, Kiener P, Langermann S;
XX
DR WPI; 2004-012002/01.
DR N-PSDB; ADE85737.
XX
PT Treating cancer or a non-cancer hyperproliferative cell disease (e.g.
PT asthma, psoriasis, inflammatory bowel disease or restenosis) in a patient
PT comprises administering to the patient a therapeutic amount of an EphA2
PT antibody.
XX
PS Disclosure; SEQ ID NO 33; 173pp; English.
XX
CC The present invention describes a method for treating cancer or a non-
CC cancer hyperproliferative cell disease or disorder in a patient, which
CC comprises administering to the patient a therapeutic amount of an EphA2
CC antibody (I) that is an EphA2 agonistic antibody, an EphA2 cancer cell
CC phenotype inhibiting antibody, an exposed EphA2 epitope antibody, or an

CC   antibody that binds EphA2 with a K-off of less than 3 x 10-3 s-1. Also
CC   described: (1) a pharmaceutical composition comprising a therapeutic
CC   amount of (I) and a pharmaceutical carrier; (2) a cell line that produces
CC   (I); (3) a hybridoma deposited with the ATCC accession number PTA-4572,
CC   PTA-4573 or PTA-4574; (4) an isolated nucleic acid comprising a
CC   nucleotide sequence encoding a light chain variable domain or a heavy
CC   chain variable domain of the EphA2 antibody; (5) a vector comprising the
CC   nucleic acid described above; (6) a host cell comprising the vector; (7)
CC   methods of identifying the EphA2 agonistic antibody or the EphA2 antibody
CC   that inhibits a cancer cell phenotype, that kills cancer cells having a
CC   cancer cell phenotype or that preferentially binds an EphA2 epitope
CC   exposed on cancer cells; and (8) a method of diagnosing, prognosing or
CC   monitoring the efficacy of therapy for cancer in a patient known to or
CC   suspected to have cancer. The composition and methods are useful
CC   in managing, diagnosing, preventing or treating hyperproliferative cell
CC   diseases (i.e. metastatic cancer) or non-cancer hyperproliferative cell
CC   diseases or disorders, such as asthma, psoriasis, inflammatory bowel
CC   disease, smooth muscle restenosis, endothelial restenosis, Crohn's
CC   disease or chronic obstructive pulmonary disease. They may also be used
CC   for monitoring the efficacy of therapy for cancer in a patient known to
CC   or suspected to have cancer, and in screening for anti-cancer drugs. The
CC   present sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 107 AA;

Query Match   98.8%; Score 556; DB 8; Length 107;
Best Local Similarity   98.1%; Pred. No. 5e-37;
Matches 105; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINNYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
               ||||||||||||||||||||||||||||:||||||||||||||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLKYDEFPYTFGGGTKLEIK 107

RESULT 2
ADL23067
ID   ADL23067 standard; protein; 107 AA.
XX
AC   ADL23067;
XX
DT   20-MAY-2004 (first entry)
XX
DE   Human EphA2 antibody VL chain.
XX
KW   antibody; human; EphA2; variable light chain; VL chain; cancer;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200401429-A2.
XX
PD   19-FEB-2004.
XX
PF   12-MAY-2003; 2003WO-US015046.
XX
PR   10-MAY-2002; 2002US-0379368P.
PR   14-OCT-2002; 2002US-0418204P.
PR   03-APR-2003; 2003US-0460358P.
XX
PA   (PURD) PURDUE RES FOUND.
XX
PI   Kinch MS, Carles-Kinch K;
XX
DR   WPI; 2004-180531/17.
DR   N-PSDB; ADL23075.
XX
PT   Treating cancer, e.g. breast, lung, prostate, or skin cancer, comprises

PT   administering an EphA2 antibody that is an EphA2 agonistic antibody or an
PT   exposed EphA2 epitope antibody.
XX
XX   Claim 49; Fig 16A, 124pp; English.
XX
CC   The present invention relates to a method of treating cancer (fully or
CC   partially refractory to a first treatment), comprising administering an
CC   EphA2 antibody that is an EphA2 agonistic antibody or an exposed EphA2
CC   epitope antibody. The method is useful for treating, managing or
CC   preventing cancer (e.g. lung, colon, prostate, breast or skin cancer),
CC   particularly metastatic cancer. The method may be used not only in
CC   untreated patients but also in the treatment of patients partially or
CC   refractory to current standard and experimental cancer therapies, e.g.
CC   chemotherapies or hormonal therapies, to improve the efficacy of such
CC   treatments. The present sequence is the human EphA2 antibody VL chain.
XX
SQ   Sequence 107 AA;

Query Match   98.8%; Score 556; DB 8; Length 107;
Best Local Similarity   98.1%; Pred. No. 5e-37;
Matches 105; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINNYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
               ||||||||||||||||||||||||||||:||||||||||||||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLKYDEFPYTFGGGTKLEIK 107

RESULT 3
ADE57549
ID   ADE57549 standard; protein; 237 AA.
XX
AC   ADE57549;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Human Protein S65921, SEQ ID NO 3411.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO200301647-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; S65921.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
XX   Claim 1; Page 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also

CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for identifying a compound which regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g.
CC   injury (CCI) and spared nerve injury; chronic constriction
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 237 AA;

Qy   ...
Db   ...

Query Match   98.4%; Score 554; DB 7; Length 237;
Best Local Similarity   99.1%; Pred. No. 1.6e-36;
Matches 106; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 82

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   83 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 129

RESULT 4
ADD47098
ID   ADD47098 standard; protein; 237 AA.
XX
AC   ADD47098;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Human Protein S65921, SEQ ID NO 12786.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0343382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (PARB) BAYER AG.
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; S65921.

New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX

CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for identifying a compound which regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g.
CC   injury (CCI) and spared nerve injury; chronic constriction
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 237 AA;

Qy   ...
Db   ...

Query Match   98.4%; Score 554; DB 7; Length 237;
Best Local Similarity   99.1%; Pred. No. 1.6e-36;
Matches 106; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 82

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   83 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 129

RESULT 5
ADD48668
ID   ADD48668 standard; protein; 237 AA.
XX
AC   ADD48668;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Human Protein S65921, SEQ ID NO 14374.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.

PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DT
DR   WPI; 2003-268312/26.
DR   GENBANK; S65921.
XX
XX
PS
XX
PT
PT
XX
Claim 1; Page; 1017pp; English.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic construction therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ   Sequence 237 AA;

Query Match   98.4%; Score 554; DB 7; Length 237;
Best Local Similarity 99.1%; Pred. No. 1.6e-36;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 23 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 82

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 83 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 129

RESULT 6
AAW35125
ID   AAW35125 standard; protein; 355 AA.
XX
AC   AAW35125;
XX
DT   20-APR-1998 ' (first entry)
XX
DE   R. pipiens recombinant RNase rOnc fusion protein 1.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
OS   Synthetic.

XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997; 97WO-US002588.
XX
PR   21-FEB-1996; 96US-0011800P.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94963.
XX
PT
XX
Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.

Disclosure; Page 67; 90pp; English.

Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nOnc and also lower immunogenicity in humans

XX
SQ   Sequence 355 AA;

Query Match   97.9%; Score 551; DB 2; Length 355;
Best Local Similarity 97.2%; Pred. No. 4e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        ||||||||||||||||||||| ::|||||||| ||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107

RESULT 7
AAW35129
ID   AAW35129 standard; protein; 355 AA.
XX
AC   AAW35129;
XX
DT   20-APR-1998 (first entry)
XX
DE   R. pipiens recombinant RNase rOnc fusion protein 5.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997; 97WO-US002588.
XX
PR   21-FEB-1996; 96US-0011800P.

```
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR  WPI; 1997-435168/40.
DR  N-PSDB; AAT94967.
XX
PT  Ribonuclease molecules based on native Onconase - used for killing cells,
PT  particularly tumour cells.
XX
PS  Disclosure; Page 71; 90pp; English.
XX
CC  Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC  (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC  novel ribonuclease molecules are highly cytotoxic and can be used alone
CC  or to form chemical conjugates or to target recombinant immunofusions.
CC  They are used particularly for decreasing tumour cell growth. They can
CC  also be used for cell separation in vitro by selectively killing unwanted
CC  types of cells, e.g. in bone marrow prior to transplantation into a
CC  patient undergoing marrow ablation by radiation, or for killing leukaemia
CC  cells or T-cells that would cause graft versus host disease. The toxins
CC  can also be used to selectively kill unwanted cells in culture. The new
CC  ribonucleases have increased cytotoxic activity compared to nOnc and also
CC  lower immunogenicity in humans
XX
SQ  Sequence 355 AA;

Qy  Query Match     97.9%;  Score 551;  DB 2;  Length 355;
Db  Best Local Similarity   97.2%;  Pred. No. 4e-36;
Matches 104;  Conservative   1;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |||||||||||||||||||||:||||||||||:|||||||||||||||||||||||||||
Db    1 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107


RESULT 8
AAW35127
ID  AAW35127 standard; protein; 358 AA.
XX
AC  AAW35127;
XX
DT  20-APR-1998 (first entry)
XX
DE  R. pipiens recombinant RNase rOnc fusion protein 3.
XX
KW  RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW  tumour cell growth; frog.
XX
OS  Rana pipiens.
OS  Synthetic.
XX
PN  WO9731116-A2.
XX
PD  28-AUG-1997.
XX
PF  19-FEB-1997;  97WO-US002588.
XX
PR  21-FEB-1996;  96US-0011800P.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR  WPI; 1997-435168/40.
DR  N-PSDB; AAT94965.
XX
PT  Ribonuclease molecules based on native Onconase - used for killing cells,
PT  particularly tumour cells.
```

```
PS  Disclosure; Page 69; 90pp; English.
XX
CC  Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC  (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC  novel ribonuclease molecules are highly cytotoxic and can be used alone
CC  or to form chemical conjugates or to target recombinant immunofusions.
CC  They are used particularly for decreasing tumour cell growth. They can
CC  also be used for cell separation in vitro by selectively killing unwanted
CC  types of cells, e.g. in bone marrow prior to transplantation into a
CC  patient undergoing marrow ablation by radiation, or for killing leukaemia
CC  cells or T-cells that would cause graft versus host disease. The toxins
CC  can also be used to selectively kill unwanted cells in culture. The new
CC  ribonucleases have increased cytotoxic activity compared to nOnc and also
CC  lower immunogenicity in humans
XX
SQ  Sequence 358 AA;

Qy  Query Match     97.9%;  Score 551;  DB 2;  Length 358;
Db  Best Local Similarity   97.2%;  Pred. No. 4e-36;
Matches 104;  Conservative   1;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |||||||||||||||||||||:||||||||||:|||||||||||||||||||||||||||
Db  119 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS 178

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||||||||||||
Db  179 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 225


RESULT 9
AAW35130
ID  AAW35130 standard; protein; 358 AA.
XX
AC  AAW35130;
XX
DT  20-APR-1998 (first entry)
XX
DE  R. pipiens recombinant RNase rOnc fusion protein 6.
XX
KW  RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW  tumour cell growth; frog.
XX
OS  Rana pipiens.
OS  Synthetic.
XX
PN  WO9731116-A2.
XX
PD  28-AUG-1997.
XX
PF  19-FEB-1997;  97WO-US002588.
XX
PR  21-FEB-1996;  96US-0011800P.
XX
PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI  Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR  WPI; 1997-435168/40.
DR  N-PSDB; AAT94968.
XX
PT  Ribonuclease molecules based on native Onconase - used for killing cells,
PT  particularly tumour cells.
XX
PS  Disclosure; Page 72; 90pp; English.
XX
CC  Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC  (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC  novel ribonuclease molecules are highly cytotoxic and can be used alone
CC  or to form chemical conjugates or to target recombinant immunofusions.
CC  They are used particularly for decreasing tumour cell growth. They can
CC  also be used for cell separation in vitro by selectively killing unwanted
```

CC   types of cells, e.g. in bone marrow prior to transplantation into a
CC   patient undergoing marrow ablation by radiation, or for killing leukaemia
CC   cells or T-cells that would cause graft versus host disease. The toxins
CC   can also be used to selectively kill unwanted cells in culture. The new
CC   ribonucleases have increased cytotoxic activity compared to nOnc and also
CC   lower immunogenicity in humans
XX
SQ   Sequence 358 AA;

Qy   Query Match   97.9%; Score 551; DB 2; Length 358;
Db   Best Local Similarity   97.2%; Pred. No. 4e-36;
     Matches 104; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   1   DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS   60
         |||||||||||||||||||||||||||||||:|||::|||||||||||||||||||||||
Db   119 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS   178

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK   107
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   179 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK   225

RESULT 10
AAW35128
ID   AAW35128 standard; protein; 360 AA.
XX
AC   AAW35128;
XX
DT   20-APR-1998 (first entry)
XX
DE   R. pipiens recombinant RNase rOnc fusion protein 4.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997; 97WO-US002588.
XX
PR   21-FEB-1996; 96US-0011800P.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94966.
XX
PT   Ribonuclease molecules based on native Onconase - used for killing cells,
PT   particularly tumour cells.
XX
PS   Disclosure; Page 70; 90pp; English.
XX
CC   Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC   (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC   novel ribonuclease molecules are highly cytotoxic and can be used alone
CC   or to form chemical conjugates or to target recombinant immunofusions.
CC   They are used particularly for decreasing tumour cell growth. They can
CC   also be used for cell separation in vitro by selectively killing unwanted
CC   types of cells, e.g. in bone marrow prior to transplantation into a
CC   patient undergoing marrow ablation by radiation, or for killing leukaemia
CC   cells or T-cells that would cause graft versus host disease. The toxins
CC   can also be used to selectively kill unwanted cells in culture. The new
CC   ribonucleases have increased cytotoxic activity compared to nOnc and also
CC   lower immunogenicity in humans
XX
SQ   Sequence 360 AA;

Query Match   97.9%; Score 551; DB 2; Length 360;
Best Local Similarity   97.2%; Pred. No. 4.1e-36;
Matches 104; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   1   DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS   60
         |||||||||||||||||||||||||||||||:|||::|||||||||||||||||||||||
Db   121 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS   180

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK   107
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK   227

RESULT 11
AAW35126
ID   AAW35126 standard; protein; 379 AA.
XX
AC   AAW35126;
XX
DT   20-APR-1998 (first entry)
XX
DE   R. pipiens recombinant RNase rOnc fusion protein 2.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997; 97WO-US002588.
XX
PR   21-FEB-1996; 96US-0011800P.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94964.
XX
PT   Ribonuclease molecules based on native Onconase - used for killing cells,
PT   particularly tumour cells.
XX
PS   Disclosure; Page 68; 90pp; English.
XX
CC   Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC   (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC   novel ribonuclease molecules are highly cytotoxic and can be used alone
CC   or to form chemical conjugates or to target recombinant immunofusions.
CC   They are used particularly for decreasing tumour cell growth. They can
CC   also be used for cell separation in vitro by selectively killing unwanted
CC   types of cells, e.g. in bone marrow prior to transplantation into a
CC   patient undergoing marrow ablation by radiation, or for killing leukaemia
CC   cells or T-cells that would cause graft versus host disease. The toxins
CC   can also be used to selectively kill unwanted cells in culture. The new
CC   ribonucleases have increased cytotoxic activity compared to nOnc and also
CC   lower immunogenicity in humans
XX
SQ   Sequence 379 AA;

Query Match   97.9%; Score 551; DB 2; Length 379;
Best Local Similarity   97.2%; Pred. No. 4.3e-36;
Matches 104; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   1   DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS   60
         |||||||||||||||||||||||||||||||:|||::|||||||||||||||||||||||
Db   143 DIKMTQSPSSMYASLGERVTFTCKASQDINNYLCWFQQKPGKSPKTLIYRANRLVDGVPS   202

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK   107

RESULT 12

Db   203   RRSGSGSGGQDYSLTISSLEYEDMGIIYYCLQYDBFPYTFGGGTKLEIK 249
          ||||||||||||||||||||||||||||||||||||||||||||||||

AAW27089
ID   AAW27089 standard; protein; 214 AA.
XX
AC   AAW27089;
XX
DT   18-NOV-1997 (first entry)
XX
DE   Mouse monoclonal antibody B9 light chain.
XX
KW   Human plasma apolipoprotein B-100; arteriosclerotic lipoprotein;
KW   antibody; Fab.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FH
FT   Region   24..34
FT   /label= CDR1
FT   Region   50..56
FT   /label= CDR2
FT   Region   89..97
FT   /label= CDR3
FT   Region   108..214
FT   /label= Ckappa
XX
PN   JP09154587-A.
XX
PD   17-JUN-1997.
XX
PF   09-MAY-1996;   96JP-0011492.
XX
PR   02-NOV-1995;   95KR-0003959459.
XX
PA   (KOAD) KOREAN SCI & TECHNOLOGY RES CENT.
XX
DR   WPI; 1997-367067/34.
DR   N-PSDB; AAT85091.
XX
PT   DNA encoding mouse antibody binding human plasma apo-lipoprotein B-100 -
PT   useful for removing arteriosclerotic lipoprotein(s).
XX
PS   Claim 4; Fig 6; 17pp; Japanese.
XX
CC   The present sequence represents the mouse monoclonal antibody B9 light
CC   chain (B9l), which binds specifically to human blood apolipoprotein B-
CC   100. The nucleic acid can be used in a method for the preparation of a
CC   reconstituted antibody which specifically binds human plasma
CC   apolipoprotein B-100. The antibody can be used as a reagent for
CC   determining the concentration of human plasma apolipoprotein B-100 in a
CC   sample. The antibody is also useful in a drug composition for selectively
CC   removing arteriosclerotic lipoproteins containing human plasma
CC   apolipoprotein B-100
XX
SQ   Sequence 214 AA;

Query Match   97.3%; Score 548; DB 2; Length 214;
Best Local Similarity   97.2%; Pred. No. 4.3e-36;
Matches 104; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVITTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||| |||:||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTTCKASQDIYSLSWFQQKPGKSPKTLIYRANRLDGVPS 60

Qy   61 RFSGSGSGGQDYSLTISSLEYEDMGIIYYCLQYDBFPYTFGGGTKLEIK 107
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGGQDYSLTISSLEYEDLGIIYYCLQFDBFPYTFGGGTKLEIK 107

RESULT 13

AAR95946
ID   AAR95946 standard; protein; 127 AA.
XX
AC   AAR95946;
XX
DT   10-FEB-1997 (first entry)
XX
DE   HNK-20 variable kappa chain.
XX
KW   Antibody; HNK-20; variable kappa chain; hybridoma; murine; IgA; mouse;
KW   F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
KW   chimeric antibody; isotype-switched antibody; therapy; infection; human;
KW   pneumonia; bronchiolitis; animal.
XX
OS   Mus musculus.
XX
PN   WO9616974-A1.
XX
PD   06-JUN-1996.
XX
PF   01-DEC-1995;   95WO-US015716.
XX
PR   01-DEC-1994;   94US-00348548.
XX
PA   (ORAV-) ORAVAX INC.
XX
PI   Berdoz J, Kraehenbuhl J;
XX
DR   WPI; 1996-286826/29.
DR   N-PSDB; AAT30456.
XX
PT   DNA encoding variable region of antibody HNK-20 - for treating
PT   respiratory syncytial virus infection.
XX
PS   Claim 9; Page 30; 75pp; English.
XX
CC   AAR95946-R95948 represent sequences for variable regions of an antibody
CC   produced by the hybridoma cell line HNK-20. This sequence represents the
CC   sequence for the antibody HNK-20 variable kappa chain. HNK-20 is a murine
CC   hybridoma cell line, that produces IgA specific for the F glycoprotein of
CC   respiratory syncytial virus (RSV). The DNA encoding these sequences were
CC   isolated using primers specific for the 5' untranslated region of the
CC   variable region, and for the intron downstream of the rearranged J region
CC   (see AAT30459-T30545 for primer sequences). The DNA encoding these
CC   sequences can be inserted into vectors containing heterologous (such as
CC   human) constant region genes, for the production of chimeric and isotype-
CC   switched antibodies. The antibodies are useful in the treatment and
CC   diagnosis of infection by RSV, such as pneumonia and bronchiolitis, in
CC   humans and animals. By using genomic DNA as a template, variable region
CC   genes can be isolated without producing fragments that have to be adapted
CC   for recombinant antibody expression. Also, by using the genomic DNA, no
CC   knowledge of the DNA sequence encoding the target variable region is
CC   required. Chimeric antibodies produced from these proteins, that contain
CC   the constant region of the host being treated, are less likely to cause
CC   adverse immune reactions
XX
SQ   Sequence 127 AA;

Query Match   97.0%; Score 546; DB 2; Length 127;
Best Local Similarity   95.3%; Pred. No. 3.7e-36;
Matches 102; Conservative   5; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||| |:|||:||:|||||||||||||||||||||||:||||
Db   21 DIKVTQSPSSMYASLGERVTTCKASQDINNYLNWFQQKPGKSPKTLIYRANRLLDGVPS 80

Qy   61 RFSGSGSGGQDYSLTISSLEYEDMGIIYYCLQYDBFPYTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 RFSGSGSGGQDYSLTISSLEYEDMGIIYYCLQFDBFPYTFGGGTKLEIK 127

RESULT 14
AAB86037

ID   AAB86037 standard; protein; 246 AA.
XX
AC   AAB86037;
XX
DT   16-JUL-2001 (first entry)
XX
DE   Murine anti-CA19-9 antigen protein.
XX
KW   Antigen; CA19-9; murine; variable heavy chain; VH; anti-CA19-9; cancer;
KW   variable light chain; VL; cytostatic; detection; stomach tumor cell;
KW   pancreas tumor cell; immunotherapy; single-chain Fv; drug targeting;
KW   prodrug activation.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   Domain   5..113
FT   /label= VH
FT   Region   114..144
FT   /note= "Linker segment"
FT   Domain   145..244
FT   /label= VL
XX
PN   EP1090927-A1.
XX
PD   11-APR-2001.
XX
PF   08-OCT-1999; 99EP-00120119.
XX
PR   08-OCT-1999; 99EP-00120119.
XX
PA   (ABKE/) ABKEN H.
XX
PI   Abken H;
XX
DR   WPI; 2001-345810/37.
DR   N-PSDB; AAF88024.
XX
PT   New single-chain Fv fragment specific for antigen CA19-9, useful for
PT   diagnosis and treatment of tumors, particularly of stomach and pancreas.
XX
PS   Claim 6; Fig 1; 23pp; German.
XX
CC   This invention describes a novel polypeptide (I), comprising an
CC   oligopeptide (OP1) having the variable region of the heavy chain (VH) of
CC   an anti-CA19-9 antibody (Ab), or its fragment with the same binding
CC   specificity for CA19-9 antigen, and an oligopeptide (OP2) based on the
CC   variable light chain (VL) region of an Ab, or its fragment, is new. OP1
CC   and OP2 are linked, directly or through a linker peptide (LP). The
CC   products of the invention have cytostatic activity. (II), optionally in
CC   radiolabeled form or fused to other active substances, is used as
CC   pharmaceutical or diagnostic agent for detection, localization and/or
CC   elimination of cells that express the CA19-9 antigen, especially stomach
CC   or pancreas tumor cells. When linked to other binding domains, (I) can be
CC   used to produce bi- or multi-specific antibodies, also useful for
CC   immunotherapy of cancers. (I), a single-chain Fv fragment, has good
CC   solubility in water, is renatured to active form very efficiently after
CC   denaturation, penetrates tissue well, and accumulates on CA19-9-
CC   presenting cells in vivo, but not on normal cells. (I) is not
CC   internalized by the cells, and has a long residence time on the cell
CC   surface, without degradation by cytoplasmic proteases, making it well
CC   suited for drug targeting, or prodrug activation. Since (I) do not
CC   include murine constant regions, it should be possible to administer them
CC   repeatedly without inducing a human anti-murine antibody response. Also,
CC   when coupled to the human CH2CH3 immunoglobulin domains, they cause
CC   specific lysis of tumor cells. This sequence represents the mouse derived
CC   anti-CA19-9 antibody construct described in the method of the invention
XX
SQ   Sequence 246 AA;

Query Match   97.0%; Score 546; DB 4; Length 246;
Best Local Similarity   97.2%; Pred. No. 7e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 137 DIQMTQSPSSMYASLGERVTTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 196

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||||||||||||||||||
Db 197 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPRTFGGGTKLEIK 243

RESULT 15
ID   AAW58505 standard; protein; 107 AA.
XX
AC   AAW58505;
XX
DT   18-AUG-1998 (first entry)
XX
DE   H65 protein sequence SEQ ID NO:26 from Fig 6.
XX
KW   Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW   depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW   autoimmune disease; rheumatoid arthritis; type I diabetes.
XX
OS   Mus sp.
XX
PN   US5770196-A.
XX
PD   23-JUN-1998.
XX
PF   23-JUN-1998.
XX
PR   07-JUN-1995; 95US-00472788.
PR   13-DEC-1991; 91US-00808464.
PR   14-DEC-1992; 92WO-US010906.
PR   23-JUN-1993; 93US-00082842.
XX
PA   (XOMA) XOMA CORP.
XX
PI   Studnicka GM;
XX
DR   WPI; 1998-376744/32.
XX
PT   Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with
PT   humanised variable regions.
XX
PS   Example 6; Col 61-64; 77pp; English.
XX
CC   A method has been developed of depleting CD5+ cells in an animal. The
CC   method comprises administering a cytotoxic protein containing a modified
CC   immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC   molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC   Ig molecule, and where the modified Ig variable domain comprises at least
CC   one of (a) a modified light chain variable region (see AAW58478 or
CC   AAW58480), and (b) a modified heavy chain variable region (see AAW58479
CC   or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65
CC   light and heavy chain variable domains with low risk amino acid
CC   substitutions [i.e. low risk of reducing antigen-binding specificity.]
CC   and AAW58480 and AAW58481 are humanised forms of the H65 light and heavy
CC   chain variable domains with moderate risk amino acid substitutions and
CC   are present in humanised H65 antibody he3 (ATCC HB 11206). The method is
CC   useful for treating autoimmune diseases, especially systemic lupus
CC   erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The
CC   present sequence represents an H65 sequence from the present invention
XX
SQ   Sequence 107 AA;

Query Match   96.1%; Score 541; DB 2; Length 107;
Best Local Similarity   96.3%; Pred. No. 7.9e-36;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db         1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60

Qy        61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
              ||||||||||||||||||| |||| |:||||||||||||
Db        61  RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDBSPWTFGGGTKLEIK 107
```

Search completed: December 29, 2004, 17:57:26
Job time : 76.5428 secs

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OM protein - protein search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.
                                      GenCore version 5.1.6

Run on: December 29, 2004, 17:38:43 ; Search time 73.8584 Seconds
                                              (without alignments)
                                              833.556 Million cell updates/sec

Sequence: 1 DIKMTQSPSSMYASLGERVT...........CLQYDEPPYTFGGGTKLEIK 107
Perfect score: 563
Title: US-10-774-076-3

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_02:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	554	98.4	236	2	Q7TS98	Q7ts98 mus musculu
2	546	97.0	214	2	Q9R1A5	Q9r1a5 mus musculu
3	534	94.8	128	2	KV5E_MOUSE	Q9r1a5 mus musculu
4	499	88.6	115	2	KV5F_MOUSE	P01637 mus musculu
5	468	83.1	236	1	Q7TMK3	P01638 mus musculu
6	398	70.7	108	1	KV1Y_HUMAN	P80362 homo sapien
7	394	70.0	108	1	KV1O_HUMAN	P01607 homo sapien
8	394	70.0	236	2	Q7Z3Y4	Q7z3y4 homo sapien
9	393	69.8	108	1	KV1B_HUMAN	P01594 homo sapien
10	392	69.6	108	1	Q9UL70	Q9ul70 homo sapien
11	391	69.4	108	1	KV1P_HUMAN	P01608 homo sapien
12	389	69.1	236	2	Q6GMX8	Q6gmx8 homo sapien
13	388	68.9	108	1	KV1V_HUMAN	P04430 homo sapien
14	384	68.2	236	2	Q6GMX9	Q6gmx9 homo sapien
15	383	68.0	108	1	KV1R_HUMAN	P01610 homo sapien
16	382	67.9	108	1	KV1A_HUMAN	P01593 homo sapien
17	382	67.9	108	1	KV1L_HUMAN	P01604 homo sapien
18	381	67.7	108	1	KV1S_MOUSE	P01648 mus musculu
19	381	67.7	108	1	KV1Q_HUMAN	P01609 homo sapien
20	380	67.5	108	1	KV5T_MOUSE	P01653 mus musculu
21	379	67.3	108	1	KV5S_MOUSE	P01652 mus musculu
22	379	67.3	298	2	Q9QYF0	Q9qyf0 synthetic c
23	378	67.2	109	2	Q96SA9	Q96sa9 homo sapien
24	378.5	67.1	109	2	Q9QYF0	Q920e6 mus musculu
25	377	67.0	236	2	Q920E6	Q6pih7 homo sapien
26	377	67.0	236	2	Q6PIH7	Q6gmw1 homo sapien
27	377	67.0	236	2	Q6GMW1	Aah34141 homo sapi
28	376	66.8	108	1	AAH34141	Kv1m_human homo sapien
29	376	66.8	108	1	KV1M_HUMAN	Kv5n_mouse mus musculu
30	376	66.8	108	1	KV5N_MOUSE	Kv5q_mouse mus musculu
31	376	66.8	236	2	Q6GMX0	Q6gmx0 homo sapien
32	375	66.6	108	2	Q9UL77	Q9ul77 homo sapien
33	374	66.4	108	1	KV1H_HUMAN	P01600 homo sapien
34	374	66.4	108	1	KV5K_MOUSE	P01644 mus musculu
35	374	66.4	111	2	AAR10992	Aar10992 mus muscu
36	373.5	66.3	107	2	KV1D_HUMAN	P01596 homo sapien
37	373	66.3	234	2	Q7Z473	Q7z473 homo sapien
38	372	66.1	108	1	KV5L_MOUSE	P01645 mus musculu
39	371.5	66.0	108	2	Q8K1F3	Q8k1f3 mus musculu
40	371	65.9	112	2	KV1C_HUMAN	P01595 homo sapien
41	371	65.9	108	1	KV5M_MOUSE	P01646 mus musculu
42	370	65.9	108	2	Q9UL79	Q9ul79 homo sapien
43	370	65.7	108	1	KV5P_MOUSE	P01649 mus musculu
44	370	65.7	130	1	KV5G_MOUSE	P01639 mus musculu
45	370	65.7	234	2	Q8R062	Q8r062 mus musculu

ALIGNMENTS

RESULT 1
ID   Q7TS98   PRELIMINARY;   PRT;   236 AA.
AC   Q7TS98;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-colorectal carcinoma light chain.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93383497; PubMed=8372513;
RA   Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT   "Cloning and characterization of 1116NS19.9 heavy and light chain
RT   cDNAs and expression of antibody fragments in Escherichia coli.";
RL   Year Immunol. 7:56-62(1993).
DR   EMBL; S65921; AAB28160.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
SQ   SEQUENCE   236 AA;   26454 MW; 2C586EBF5EA10F4C CRC64;

Query Match   98.4%; Score 554; DB 2; Length 236;
Best Local Similarity   99.1%; Pred. No. 1.9e-49;
Matches 106; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   23 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 82

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPPYTFGGGTKLEIK 107
               |||||||||||||||||||||||||||||||||||||||||||||||
Db   83 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPPRTFGGGTKLEIK 129

RESULT 2
Q9R1A5
ID   Q9R1A5   PRELIMINARY;   PRT;   214 AA.
AC   Q9R1A5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Kappa light chain of Mab7 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF152371; AAD40242.1; -.
DR   PIR; PH1065; PH1065.
DR   PDB; 1AHW; X-ray; D=--.
DR   PDB; 1CIC; X-ray; A/C=1-214.
DR   PDB; 1E08; X-ray; A/C=1-214.
DR   PDB; 1K6Q; X-ray; L=1-210.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
KW   Immunoglobulin V region; Homeobox.
FT   SIGNAL
FT   CHAIN
FT   DOMAIN
FT   DOMAIN
FT   DOMAIN
FT   DOMAIN
FT   DOMAIN
FT   DOMAIN
FT   DOMAIN
FT   DISULFID
FT   NON_TER   1
FT   NON_TER   214
SQ   SEQUENCE   214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match   97.0%;
Best Local Similarity   96.3%;
Matches 103;   Conservative   3;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPFYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPFPTFGSGTKLEIK 107

RESULT 3
ID   KV5B_MOUSE   STANDARD;   PRT;   128 AA.
AC   P01637;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region T1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN   [1]
RX   MEDLINE=81052342; PubMed=6776411;
RA   Altenburger W., Steinmetz M., Zachau H.G.;
RT   "Functional and non-functional joining in immunoglobulin light chain
RT   genes of a mouse myeloma.";
RL   Nature 287:603-607(1980).

DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS50835; IG_V; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   128
FT   DOMAIN   21   128   Ig kappa chain V-V region T1.
FT   DOMAIN   21   43   Framework-1.
FT   DOMAIN   44   54   Complementarity-determining-1.
FT   DOMAIN   55   69   Framework-2.
FT   DOMAIN   70   76   Complementarity-determining-2.
FT   DOMAIN   77   108   Framework-3.
FT   DOMAIN   109   117   Complementarity-determining-3.
FT   DOMAIN   118   127   Framework-4.
FT   DISULFID   43   108   By similarity.
FT   NON_TER   128   128
SQ   SEQUENCE   128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

Query Match   94.8%;
Best Local Similarity   93.5%;
Matches 100;   Conservative   5;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |||||||||||||||||:|:|||||||||||||||||||||||||||||||||||||||
Db 21 DIKMTQSPSSMYASLGERVTISCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 80

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPFYTFGGGTKLEIK 107
        |||||||||||||||||||||||||||:|:||||||||||||||||||
Db 81 RFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGAGTKLEIK 127

RESULT 4
ID   KV5F_MOUSE   STANDARD;   PRT;   115 AA.
AC   P01638;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region L6 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN   [1]
RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
DR   PIR; A01921; KVMSL6.
DR   HSSP; P01607; 1BWW.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL   1   20
FT   CHAIN   21   >115
FT   DOMAIN   21   43   Framework-1.
FT   DOMAIN   44   54   Complementarity-determining-1.
FT   DOMAIN   55   69   Framework-2.
FT   DOMAIN   70   76   Complementarity-determining-2.
FT   DOMAIN   77   108   Framework-3.
FT   DOMAIN   109   >115   Complementarity-determining-3.
FT   DISULFID   43   108   By similarity.
FT   NON_TER   115   115
SQ   SEQUENCE   115 AA; 12986 MW; BA852C58F328B1C3 CRC64;

Query Match   88.6%;   Score 499;   DB 1;   Length 115;

```
Qy    1 DIKMTQSPSSMYASLGERVITTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 DIKMTQSPSSMYASLGERVITTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFP 95
        ||||||||||||||||||||||||||||||||||||
Db   81 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFP 115
```

RESULT 5

Best Local Similarity 100.0%; Pred. No. 4.5e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID   Q7TMK3   PRELIMINARY;   PRT;   236 AA.
AC   Q7TMK3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFP 95
        ||||||||||||||||||||||||||||||||||||
Db   81 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFP 115
```

RESULT 6

ID   KV1Y_HUMAN   STANDARD;   PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Brunger A.T., Bulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PDB; 1WTL; X-ray; A/B=1-108.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN   1   23   Framework-1.
FT   DOMAIN   24   34   Complementarity-determining-1.
FT   DOMAIN   35   49   Framework-2.
FT   DOMAIN   50   56   Complementarity-determining-2.
FT   DOMAIN   57   88   Framework-3.
FT   DOMAIN   89   97   Complementarity-determining-3.
FT   DOMAIN   98   107   Framework-4.
FT   DISULFID   23   88   By similarity.
FT   CONFLICT   4   7   TN -> SD (in Ref. 2).
FT   STRAND   10   13
FT   STRAND   15   16
FT   TURN   19   25
FT   STRAND   30   31
FT   TURN   33   38
FT   STRAND   40   41
FT   STRAND   45   49
FT   TURN   50   52
FT   STRAND   53   54
FT   STRAND   56   57
FT   TURN   60   61
FT   STRAND   62   67
FT   TURN   68   69
FT   STRAND   70   75

```
Qy   23 DIKMTQSPSSMYASLGERVITTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 82
        |||| ||||||||||||||||||||||||||||||||||||||| ||||| ||| ||||| 
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFPYTFGGGTKLEIK 107

Qy   83 RFSGSGSGQDYSLTISSLESDDTATYYCLQHGESPYTFGSGTKLEIK 129
        ||||||||||||||||||   | |||||||  |||||||| |||||| 
Db   83 RFSGSGSGQDYSLTISSLESDDTATYYCLQHGESPYTFGSGTKLEIK 129
```

Best Local Similarity 85.0%; Pred. No. 1.8e-40;
Matches 91; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

```
Qy    1 DIKMTQSPSSMYASLGERVITTCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
```

Left column (RESULT 7)

```
FT   HELIX          80     82
FT   STRAND         84     90
FT   STRAND         98     98
FT   STRAND        102    106
FT   NON_TER       108    108
SQ   SEQUENCE    108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;
```

Query Match   70.7%;   Score 398; DB 1; Length 108;
Best Local Similarity   68.2%;   Pred. No. 1.4e-33;
Matches   73; Conservative   18; Mismatches   16; Indels   0; Gaps   0;

```
Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |:|:||||||| :: ||||||||:||||| :||:||||:|||:||:|||  ||:| |||
Db    1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        |||||||| |  | ||||  ||: |||| ||||   |||||||:|||
Db   61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107
```

RESULT 7
```
ID   KV10_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
-!-  MISCELLANEOUS: The C region of this chain has the INV (1,2)
     marker.
-!-  MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!-
DR   PIR; A91663; KIHURE.
DR   PDB; 1A2R; X-ray; @=1-107.
DR   PDB; 1BWW; X-ray; A/B=1-107.
DR   PDB; 1REI; X-ray; A/B=1-107.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN         1     23       Framework-1.
FT   DOMAIN        24     34       Complementarity-determining-1.
FT   DOMAIN        35     49       Framework-2.
FT   DOMAIN        50     56       Complementarity-determining-2.
FT   DOMAIN        57     88       Framework-3.
FT   DOMAIN        89     97       Complementarity-determining-3.
```

Right column (RESULT 8)

```
FT   DOMAIN        98    107       Framework-4.
FT   DISULFID      23     88
FT   STRAND         4      7
FT   STRAND        10     13
FT   TURN          15     16
FT   STRAND        19     25
FT   TURN          30     31
FT   STRAND        33     38
FT   TURN          40     41
FT   STRAND        45     49
FT   TURN          50     52
FT   STRAND        53     54
FT   TURN          56     57
FT   STRAND        60     61
FT   STRAND        62     67
FT   STRAND        68     69
FT   HELIX         70     75
FT   STRAND        80     82
FT   HELIX         84     90
FT   STRAND        97     98
FT   STRAND       102    106
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;
```

Query Match   70.0%;   Score 394; DB 1; Length 108;
Best Local Similarity   69.8%;   Pred. No. 3.7e-33;
Matches   74; Conservative   13; Mismatches   19; Indels   0; Gaps   0;

```
Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |:|:|||||| :: |:  |||||:||||| :||:| |||:|||:|||:||| : | ||||
Db    1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEI 106
        |||||||| | :| ||||  ||: ||||   | : | |||||||:|
Db   61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGGGTKLQI 106
```

RESULT 8
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ID   Q72ZY4     PRELIMINARY;      PRT;   236 AA.
AC   Q72ZY4;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal Muscle;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005332; AAH05332.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match   70.0%; Score 394; DB 2; Length 236;
Best Local Similarity   69.2%; Pred. No. 9e-33;
Matches   74; Conservative   16; Mismatches   17; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |:|||||||||:|||:|||:|||||||||||||:|||||||||:|||::|||||||||||
Db   23 DIQMTQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDBFPYTFGGGTKLEIK 107
              |||||||||:||||:|||||:|||| |||||:|||:||||||||||||
Db   83 KFSGSGSGTDTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIK 129

RESULT 9
ID   KV1B_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the Bence-
RT   Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: The structure of the V region was determined by
CC   molecular replacement methods using the known structure of the V
CC   region of the kappa chain RBI.
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91653; KIHUAU.
DR   PDB; 1JVS; X-ray; A=1-107.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN   1   107   Immunoglobulin V region.
FT   DOMAIN   1   23   Framework-1.
FT   DOMAIN   24   34   Complementarity-determining-1.
FT   DOMAIN   35   49   Framework-2.
FT   DOMAIN   50   56   Complementarity-determining-2.
FT   DOMAIN   57   88   Framework-3.
FT   DOMAIN   89   97   Complementarity-determining-3.
FT   DOMAIN   98   107   Framework-4.
FT   DISULFID   23   88   By similarity.
FT   STRAND   4   5
FT   STRAND   10   13
FT   TURN   15   16
FT   STRAND   16   25
FT   STRAND   19   25
FT   STRAND   30   31
FT   STRAND   33   38
FT   TURN   40   41
FT   STRAND   44   49
FT   TURN   50   52
FT   STRAND   53   54
FT   TURN   56   57
FT   STRAND   60   61
FT   TURN   62   67
FT   STRAND   68   69
FT   STRAND   70   75
FT   HELIX   80   82
FT   STRAND   85   90
FT   STRAND   97   98
FT   STRAND   102   106
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11939 MW; E80111B7EB6F6FB9 CRC64;

Query Match   69.8%; Score 393; DB 1; Length 108;
Best Local Similarity   68.2%; Pred. No. 4.7e-33;
Matches   73; Conservative   16; Mismatches   18; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |:|||||||||:|||:||||:|||||||||||:|||:|||||||:|||:||| ::|||||
Db   1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKRAPKLLIYDASNLESGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDBFPYTFGGGTKLEIK 107
              ||||.||| :.|:|||||:|||| ||||||||::|| ||||||||:||
Db   61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWFGQGTKVBIK 107

RESULT 10
ID   Q9UL70   PRELIMINARY;   PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035044; AAD5280.1; -.
DR   PIR; PH0863; PH0863.
DR   HSSP; P01607; 1BWW.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.

```
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3B41FCCA37 CRC64;

Qy   Query Match    69.6%;  Score 392;  DB 2;  Length 108;
     Best Local Similarity  69.2%;  Pred. No. 5.9e-33;
     Matches  74;  Conservative  17;  Mismatches  16;  Indels  0;  Gaps  0;

Qy    1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
         ||||||:|||| :||:|.:||||||:|||::|||.:|||||||:.|:|||| . ::.|||
Db    1  DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy   61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
         |||||||| |::|||||| ::|:. |||||::...||||| ||||:||
Db   61  RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107


RESULT 11
ID   KV1P_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL   York (1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91638; KIHURY.
DR   HSSP; P01607; 1BWW.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER       1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACBE8A31DF3A CRC64;

Qy   Query Match    69.4%;  Score 391;  DB 1;  Length 108;
     Best Local Similarity  66.4%;  Pred. No. 7.5e-33;
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```
Matches   71;  Conservative  20;  Mismatches  16;  Indels  0;  Gaps  0;

Qy    1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
         ||||||:||||   :|.:||||||:|||::.:.|.:|||||||.:||.||||||.:|..|||
Db    1  DIQMTQSPSSLSASVGDRVTITCRASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy   61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
         |||| |||||::|||||| ::|:| ||||::...||||||||||:|:|
Db   61  RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107


RESULT 12
ID   Q6GMX8
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; Ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B559EFC9 CRC64;

Qy   Query Match    69.1%;  Score 389;  DB 2;  Length 236;
     Best Local Similarity  68.2%;  Pred. No. 3e-32;
     Matches  73;  Conservative  17;  Mismatches  17;  Indels  0;  Gaps  0;

Qy    1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
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```
Db        23  DIQMTQSPSSVSASVGDRVTITCRASQGISSWIAWYQQKPGKAPKLLIYAASSLQSGVPS  82
              |||: |||||||  |||: |||  ||||    |  |||:|||| ||   |||| :|  |||
Qy        61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGQGTKLEIK  107
              ||||||||    ||||| ||:|||| |||||  ||: |: |||||||
Db        83  RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSFPFITFGPGPKVDIK  129
```

RESULT 13

<pre>
ID   KV1V_HUMAN   STANDARD;   PRT;   108 AA.
AC   P04430;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region BAN.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86174817; PubMed=3083240;
RA   Dwulet F.E., O'Connor T.P., Benson M.D.;
RT   "Polymorphism in a kappa I primary (AI) amyloid protein (BAN).";
RL   Mol. Immunol. 23:73-78(1986).
RN   [2]
HSSP; A01878; 1KIHUBN.
PIR; A01878; 1WTL.
DR   PIR; A01878; 1WTL.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN   1   23   Framework-1.
FT   DOMAIN   24   34   Complementarity-determining-1.
FT   DOMAIN   35   49   Framework-2.
FT   DOMAIN   50   56   Complementarity-determining-2.
FT   DOMAIN   57   88   Framework-3.
FT   DOMAIN   89   97   Complementarity-determining-3.
FT   DOMAIN   98   107   Framework-4.
FT   DISULFID   23   88   By similarity.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
```

<pre>
Query Match             68.9%;  Best Local Similarity   65.4%;
Matches  70;  Conservative  20;  Mismatches  17;  Indels   0;  Gaps   0;
                        Score 388;  DB 1;  Length 108;
                        Pred. No. 1.5e-32;
</pre>

```
Qy         1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60
              |||||||||| :||| |||||||| ||||||||| ||:|||||| :||| |||||||||
Db         1  DIQLTQSPSSLSASVGDRVTITCRASQSVNYVAWFQQKPGKAPKSLIYDASTLQSGVPS  60
Qy        61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGQGTKLEIK  107
              |||||||||   ||||| || |:||| |||||| |: |::||||| |
Db        83  RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK  107
```

RESULT 14

<pre>
ID   Q6GMX9_HUMAN   PRELIMINARY;   PRT;   236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073763; AAH73763.1; -.
DR   EMBL; BC073763; AAH73763.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
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<pre>
Query Match   68.2%; Best Local Similarity   65.4%;
Matches 70; Conservative 20; Mismatches 17; Indels   0; Gaps   0;
                        Score 384; DB 2; Length 236;
                        Pred. No. 9.9e-32;
</pre>

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Qy         1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60
              ||||||||| :||| |||||||:|||||||| |:||:|||||| :| ||||||||| ||
Db        61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGQGTKLEIK  107
              ||||||||    |||||||:|:|||| |||||  ||:|::|||||:||
Db        83  RFSGSGSGTDFTLTISSLQPEDFATYYCQQVNTYPLTFGQGTKVEIK  129
```

RESULT 15

<pre>
ID   KV1R_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region WEA.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
```

```
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT   in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC       against 3,4-pyruvylated galactose and isolated from a patient with
CC       Waldenstrom's macroglobulinemia.
DR   PIR; A01876; KIHUWE.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Monoclonal antibody.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11840 MW;  9249B61F0945618C CRC64;

Query Match             68.0%;  Score 383;  DB 1;  Length 108;
Best Local Similarity   66.4%;  Pred. No. 5.1e-32;
Matches   71;  Conservative   17;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |:||||||||:|||||||||||||:||||||||:|||:|||||||||||:||::||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVPS 60

Qy         61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPFYTFGGGTKLEIK 107
              ||||||||:.:||||||:||||:|| ||||||| ||:|| |||:|:|
Db         61 RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEVK 107
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 14,677 Seconds
(without alignments)
701.451 Million cell updates/sec

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Title: US-10-774-076-3
Perfect score: 563
Sequence: 1 DIKMTQSPSSMYASLGERVT.........CLQYDEFPYTFGGGTKLEIK 107
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Database : PIR.79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 283416

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	546	97.0	127	2	S52447	Ig kappa chain V r
2	534	94.8	128	1	KVMST1	Ig kappa chain pre
3	525	93.3	234	2	S14237	Ig kappa chain pre
4	519	92.2	128	2	PL0101	Ig kappa chain pre
5	506	89.9	106	2	S20652	Ig kappa chain V r
6	499	88.6	115	2	KVMSL6	Ig kappa chain pre
7	487	86.5	98	2	PH1065	Ig kappa chain pre
8	460	81.7	104	2	S13700	Ig kappa chain V r
9	440	78.2	103	2	S13703	Ig kappa chain V r
10	412	73.2	129	2	B23986	Ig kappa chain pre
11	410	72.8	101	2	S13701	Ig kappa chain V r
12	410	72.8	129	2	S52789	Ig kappa chain V r
13	399	70.9	75	2	A34966	Ig heavy chain V r
14	397	70.5	107	2	S36264	Ig lambda chain V
15	397	70.5	132	2	S40369	Ig kappa chain - h
16	397	70.5	132	2	S40334	Ig kappa chain - h
17	395	70.2	125	2	S40316	Ig kappa chain - h
18	394	70.0	108	1	K1HURE	Ig kappa chain V-I
19	394	70.0	125	2	S40333	Ig kappa chain V-J
20	393	69.8	108	1	K1HUAU	Ig kappa chain V-I
21	393	69.8	108	1	I39154	Ig kappa chain (BR
22	393	69.8	108	2	B49047	Ig kappa chain V r
23	392.5	69.7	106	2	C33936	Ig kappa chain V r
24	392	69.6	108	1	S19674	Ig kappa chain V r
25	391	69.4	108	1	K1HURY	Ig kappa chain V-I
26	391	69.1	123	2	S40313	Ig kappa chain V-I
27	389	69.1	131	2	S40352	Ig kappa chain V-J
28	388.5	69.1	104	2	S26329	Ig kappa chain V-J
29	388	68.9	108	1	K1HUBN	Ig kappa chain V-I
30	388	68.9	125	2	S09365	Ig kappa chain - m
31	388	68.6	107	2	B49026	Ig kappa chain V r
32	386	68.6	108	2	S19912	Ig kappa chain V-J
33	386	68.6	125	2	S40349	Ig kappa chain V-J
34	386	68.4	108	2	S19970	Ig kappa chain V r
35	385	68.4	127	2	PH1224	Ig kappa chain V r
36	385	68.4	117	2	S46371	Ig kappa chain V-J
37	384	68.2	123	2	S40331	Ig kappa chain V r
38	384	68.2	129	2	S40017	Ig kappa chain - h
39	383.5	68.1	104	2	S26330	Ig kappa chain V-J
40	383	68.0	108	1	K1HUWE	Ig kappa chain V r
41	383	68.0	110	2	S44118	Ig kappa chain V-J
42	383	68.0	125	2	S40350	Ig kappa chain V-J
43	382.5	67.9	108	2	S36275	Ig lambda chain V
44	382	67.9	107	2	K1HUAG	Ig kappa chain V-I
45	382	67.9	108	1	K1HUKU	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S52447
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52447
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged ge
A;Cross-references: EMBL:X82688; NID:g673443; PIDN:CAA58009.1; PID:g673444
C;Genetics:
A;Reference number: S52447
A;Accession: S52445
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-127 <BER>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 97.0%; Score 546; DB 2; Length 127;
Best Local Similarity 95.3%; Pred. No. 1.7e-39;
Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
         ||||:|||||||||||||||||||||||:||||:||:||||||||||||||||:|||||
Db 21 DIKVTQSPSSMYASLGERVTITCKASQDINNYLNWFQQKPGKSPKTLIYRANRLLDGVPS 80

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
         |||||||||||||||||||||||||||||:||||||||||||||
Db 81 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQFDEFPYTFGGGTKLEIK 127

RESULT 2
KVMST1
Ig kappa chain precursor V region (T1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1980 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
C;Accession: A01920
R;Altenburger, W.; Steinmetz, M.; Zachau, H.G.
Nature 287, 603-607, 1980
A;Title: Functional and non-functional joining in immunoglobulin light chain genes of a
A;Reference number: A01920; MUID:81052342; PMID:6776411
A;Accession: A01920
A;Molecule type: mRNA
A;Residues: 1-128 <ALT>
A;Cross-references: UNIPROT:P01637; GB:V00772; NID:g951636; PIDN:CAA24150.1; PID:g762975
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-128/Product: Ig kappa chain V region; immunoglobulin homology
F;36-110/Domain: immunoglobulin V region; immunoglobulin homology <IMM>
F;43-108/Disulfide bonds: #status predicted

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Query Match             94.8%;   Score 534;  DB 1;  Length 128;
Best Local Similarity   93.5%;   Pred. No. 1.7e-38;
Matches  100;  Conservative   5;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPLTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||||:||:|
Db   81 RFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGAGTKLELK 127
```

RESULT 3
S14237

Ig kappa chain precursor (15C5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S14237
R;Near, R.I.; Haber, E.
Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibody d
A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Accession: S14237
A;Molecule type: mRNA
A;Residues: 1-234 <VAN>
C;Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623
C;Superfamily: immunoglobulin; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

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Query Match             91.6%;   Score 525;  DB 2;  Length 234;
Best Local Similarity   91.6%;   Pred. No. 1.8e-37;
Matches   98;  Conservative   5;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 DIKMTQSPSSMYASLGERVTVTCKASQDINSYLSWIQQKPGKSPKTLIYRGNRLVAGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          |||||||||||||||||||||||||||||||||||||:||||||||
Db   81 RFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGAGTKLELK 127
```

RESULT 4
PL0101

Ig kappa chain precursor V region (40-140) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0101
R;Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A;Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding seq
A;Reference number: A93255; MUID:81220975; PMID:6264318
A;Accession: A01921
A;Molecule type: DNA
A;Residues: 1-115 <PEC>
A;Cross-references: UNIPROT:P01638; GB:V01563; GB:J00573; NID:g51714; PIDN:CAA24883.1;
A;Note: the sequence was determined from the germline gene
A;Genetics:
A;Introns: 17/1

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Query Match             89.9%;   Score 506;  DB 2;  Length 106;
Best Local Similarity   89.6%;   Pred. No. 3.4e-36;
Matches   95;  Conservative   7;  Mismatches   4;  Indels   0;  Gaps   0;

Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLNWFQQKPGRSPRTLIYRSNRLVHGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDFFPYTFGGGTKLEI 106
          |||||||||||||||||||||||||||||||:|||:||||||||||
Db   61 RFSGSGSGLYFSLSISSLEYEDMGIYFCLQYDDFPPYTFGSGTKLEI 106
```

RESULT 6
KVMSL6

Ig kappa chain precursor V region (L6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A01921
R;Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A;Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding seq
A;Reference number: A93255; MUID:81220975; PMID:6264318
A;Accession: A01921
A;Molecule type: DNA
A;Genetics:
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region (L6) #status predicted <IMM>
F;36-110/Domain: immunoglobulin V region; immunoglobulin homology
F;43-108/Disulfide bonds: #status predicted

C;Superfamily: immunoglobulin; immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;36-110/Domain: immunoglobulin homology <IMM>
F;115-128/Domain: J segment #status predicted <JRE>

```
Query Match             92.2%;   Score 519;  DB 2;  Length 128;
Best Local Similarity   92.5%;   Pred. No. 3.2e-37;
Matches   99;  Conservative   3;  Mismatches   5;  Indels   0;  Gaps   0;

Qy    1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRTKRLVDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          ||||||||||||||||||||||||||||||||:|
Db   81 RFSGSGSGQDYSLTISSLEYEDMGIYFCLQYDEFPLTFGAGTKLELK 127
```

RESULT 5
S20652

Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20652
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice reac
A;Accession: S20652
A;Molecule type: DNA
A;Reference number: S20639
A;Status: preliminary
A;Accession: S20652
A;Residues: 1-106 <LOS>
A;Cross-references: EMBL:X65008; NID:g52649; PIDN:CAA46141.1; PID:g52650
C;Superfamily: immunoglobulin; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```
Query Match             92.2%;   Score 519;  DB 2;
```

Query Match   88.6%; Score 499; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 80

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDEFPYP 95
      |||||||||||||||||||||||||||||||||||||
Db 81 RFSGSGSGGQDYSLTISSLEYEDMGIIYCLQYDEFP 115
```

RESULT 7
PH1065
Ig kappa chain V region (clone 163.47) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PH1065
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92281444; PMID:1512540
A;Accession: PH1065
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98 <TIL>
A;Cross-references: UNIPROT:Q9R1A5
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Query Match   86.5%; Score 487; DB 2; Length 98;
Best Local Similarity   94.9%; Pred. No. 1.3e-34;
Matches 93; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy  1 DIKMTQSPSSMYASLGERVTITCKASQDINNYLSWFQQIPGKSPKTLIYRAKRLVDGVPS 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1 DIKMTQSPSSMYASLGERVTITCKASQDINNYLSWFQQIPGKSPKTLIYRAKRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDEFPYTF 98
      |||||||||||||||||||||||||||||||||||||
Db 61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLHYDEFPYTF 98
```

RESULT 8
S13700
Ig kappa chain V region (hybridoma NC19-E10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S13700, S13702
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13700
A;Molecule type: mRNA
A;Residues: 1-99 <PB2>
A;Experimental source: hybridoma NC19-F5
A;Cross-references: EMBL:X53355; NID:g55308; PIDN:CAA37441.1; PID:g930226
A;Accession: S13702
A;Molecule type: mRNA
A;Residues: 1-104 <PEN>
A;Experimental source: hybridoma NC19-E10
A;Cross-references: EMBL:X53353; NID:g55304; PIDN:CAA37439.1; PID:g930224
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match   81.7%; Score 460; DB 2; Length 104;
Best Local Similarity   85.6%; Pred. No. 2.6e-32;
Matches 89; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

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Qy  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
      ||||||||||||||||||||||||||||| ||||||||| ||||||||||  | ||||||
Db  1 DIKMTQSPSSMYASLGERVTITCKASQDIKSYLSWFQQKPWKSPKTLIYYATSLADGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDEFPYTFGGGTKL 104
      |||||||||||||||||||  |    | |||  | |||||||||
Db 61 RFSGSGSGQDYSLTISSLESDDTATYYCLQHGESPYTFGGGTKL 102
```

RESULT 9
S13703
Ig kappa chain V region (hybridoma NC17-D8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S13703
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13703
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <PEN>
A;Cross-references: EMBL:X53356; NID:g55310; PIDN:CAA37442.1; PID:g930227
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   83.3%; Score 440; DB 2; Length 103;
Best Local Similarity   78.2%; Pred. No. 1.3e-30;
Matches 85; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

```
Qy  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
      ||||||||||||||||||||||||||||| |||||||||||||||||||  ||||||||
Db  1 DIKMTQSPSSMYASLGERVTITCKASQDIKSYLSWFQQKPGKSPKTLIYYATSLADGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDEFPYTFGGGT 102
      |||||||||||||||||||  |    | |||  | |||||||
Db 61 RFSGSGSGQDYSLTISSLESDDTATYYCLQHGESPYTFGGGXT 102
```

RESULT 10
B23986
Ig kappa chain precursor V region (IR2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 21-Jan-2000
C;Accession: B23986
R;Hellman, L.; Engstrom, A.; Bennich, H.; Pettersson, U.
Gene 40, 107-114, 1985
A;Title: Structure and expression of kappa-chain genes in two IgE-producing rat immunoc
A;Reference number: A91541; MUID:86137406; PMID:3005117
A;Accession: B23986
A;Molecule type: mRNA
A;Residues: 1-129 <HEL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   73.2%; Score 412; DB 2; Length 129;
Best Local Similarity   72.9%; Pred. No. 3.7e-28;
Matches 78; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

```
Qy  1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
      || ||||||||| | | | |||  |||| |   | |||||||  | |||||| |  ||||
Db 23 DIQMTQSPSSMSVSVGDRVTIPCRASQDVGIVIWFQQKPGRRIYLYLATTLADGVPS 82

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107
      |||| ||| ||||||||||    |   | ||   | |||| ||| |||
Db 83 RFSGSKSGSDYSLTISSLESEBVADYHCLQVNEYPYTFGPGTKLELK 129
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Query Match   81.7%; Score 460; DB 2; Length 104;

RESULT 11
S13701
Ig kappa chain V region (hybridoma NC19-E11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
A;Molecule type: mRNA
A;Residues: 1-101 <PEN>
A;Cross-references: EMBL:X53354
A;Accession: S13701
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89328557; PMID:2503389
A;Accession: S13701
A;Status: Preliminary
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match   72.8%; Score 410; DB 2; Length 101;
Best Local Similarity   80.2%; Pred. No. 4.3e-28;
Matches   81; Conservative   2; Mismatches   18; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |||||||||||||||||||||||||||||||||||| | |: :|||||
Db   1 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWYQQKPWKSPKTLIYATSLADGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQVDEFPYTFGGG 101
        ||||||| ||||||||||| ||: |||| ||||||||
Db 61 RFSGSGSGXDYSLTISSLESDDTATXXCXXXGESPYTFGGG 101

RESULT 12
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
A;Molecule type: mRNA
A;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Keywords: immunoglobulin; immunoglobulin homology
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match   71.0%; Score 410; DB 2; Length 129;
Best Local Similarity   76; Conservative   16; Pred. No. 5.4e-28;
Matches   76; Conservative   16; Mismatches   15; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        ||||||||||:|||||||||||||||||||||| |||||||||||| :::||||
Db 23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIHAASSLETGVPS 82

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        ||||||| ||||||||| :::||||| :||| |||||||| ||||
Db 83 RFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGGGTKVEIK 129

RESULT 13
A34966
Ig heavy chain V region (PR8-9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-1991 #sequence_revision 23-Jul-1999
A;Molecule type: mRNA
C;Accession: A34966
R;Caton, A.J.; Koprowski, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 6450-6454, 1990
A;Title: Influenza virus hemagglutinin-specific antibodies isolated from a combinatorial

A;Reference number: A34966; MUID:90349634; PMID:1696733
A;Accession: A34966
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-75 <CAT>
A;Cross-references: GB:M57280; NID:g197784; PIDN:AAA39155.1; PID:g197785
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match   70.9%; Score 399; DB 2; Length 75;
Best Local Similarity   97.3%; Pred. No. 2.7e-27;
Matches   73; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy 30 NSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCL 89
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   1 NSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCV 60

Qy 90 QYDEFPYTFGGGTKL 104
        ||||:||||||||||
Db 61 QYDEYPYTFGGGTKL 75

RESULT 14
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36264
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36264
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match   70.5%; Score 397; DB 2; Length 107;
Best Local Similarity   73; Conservative   17; Pred. No. 5.7e-27;
Matches   73; Conservative   17; Mismatches   17; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        ||||||||||:||:|||:||||| ||||||| |||||||||||||| :::||||
Db   1 EIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        ||||||| ||||||||| :::||||| :||| |||||||| ||||
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNPLTFGGGTKVDIK 107

RESULT 15
S40369
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40369
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40369
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match   68.2%; Score 397; DB 2; Length 107;
Best Local Similarity   73; Conservative   17; Pred. No. 5.7e-27;
Matches   73; Conservative   17; Mismatches   17; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVIITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        ||||||||||:||:|||:||||| ||||||| |||||||||||||| :::||||
Db   1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
        ||||||| ||||||||| :::||||| :||| |||||||| ||||
Db 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNPLTFGGGTKVDIK 107

Query Match   70.5%;   Score 397; DB 2;   Length 129;
Best Local Similarity 69.2%;   Pred. No. 6.8e-27;
Matches 74; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
          ||:||||||||:||:|||||||:|||||||:||||:|||||||||||||||:|:||||||
Db   22 DIQMTQSPSSLSASVGDRVTITCRASHVISNHLVWFQQKPGKAPKSLIYAASSLQSGVPS 81

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
          :||||||||:|:||||||||| ||| |||:||||||||||||||||
Db   82 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPYTFGQGTKLEIK 128

Search completed: December 29, 2004, 18:06:56
Job time : 15.8437 secs

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 29, 2004, 18:05:34 ; Search time 61.8643 Seconds
                                            (without alignments)
                                            622.182 Million cell updates/sec

Title: US-10-774-076-3
Perfect score: 563
Sequence: 1 DIKMTQSPSSMYASLGERVT...........CLQYDEPFYTFGGGTKLEIK 107

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Post-processing: Minimum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Published_Applications_AA:*
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               9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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              11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
              12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
              13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
              14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
              15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
              16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
              17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
              18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
              19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
              20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	563	100.0	107	17	US-10-774-076-3	Sequence 3, Appli
2	563	100.0	127	17	US-10-774-076-11	Sequence 11, Appl
3	556	98.8	107	15	US-10-436-782-33	Sequence 33, Appl
4	556	98.8	107	15	US-10-436-783-1	Sequence 1, Appli
5	541	96.1	107	14	US-10-340-189-26	Sequence 26, Appl
6	541	96.1	107	15	US-10-325-696-26	Sequence 26, Appl
7	531	94.3	107	14	US-10-127-890-123	Sequence 123, App
8	527	93.6	107	9	US-09-158-120A-21	Sequence 21, Appl
9	522	92.7	142	9	US-09-797-481-2	Sequence 2, Appli
10	522	92.7	142	9	US-09-844-736-4	Sequence 4, Appli
11	522	92.7	142	14	US-09-162-396-4	Sequence 4, Appli
12	522	92.7	142	17	US-10-819-693-4	Sequence 4, Appli
13	508	90.2	107	14	US-10-340-189-27	Sequence 27, Appl
14	508	90.2	107	15	US-10-325-696-27	Sequence 27, Appl1
15	503	89.3	107	14	US-10-774-076-14	Sequence 14, Appl
16	503	89.3	127	17	US-10-774-076-19	Sequence 19, Appl
17	487	86.5	107	14	US-10-127-890-125	Sequence 125, Appl
18	487	86.5	107	14	US-10-340-189-87	Sequence 87, Appl
19	487	86.5	107	15	US-10-325-696-65	Sequence 65, Appl1
20	484	86.0	240	14	US-10-127-890-147	Sequence 147, App
21	484	86.0	240	14	US-10-127-890-148	Sequence 148, App
22	465	82.6	107	15	US-10-412-406-1	Sequence 1, Appli
23	465	82.6	4852	15	US-10-412-406-33	Sequence 33, Appl
24	464	82.4	107	16	US-10-462-062-148	Sequence 148, App
25	464	82.4	107	15	US-10-472-905A-100	Sequence 100, App
26	464	82.4	127	16	US-10-462-062-162	Sequence 162, App
27	464	82.4	127	15	US-10-472-905A-104	Sequence 104, App
28	463	82.2	107	16	US-10-462-062-147	Sequence 147, App
29	463	82.2	129	15	US-10-472-905A-161	Sequence 161, App
30	458	81.3	107	9	US-09-158-120A-20	Sequence 20, Appl
31	458	81.3	251	15	US-10-239-656-65	Sequence 65, Appl
32	447	79.4	127	16	US-10-462-062-107	Sequence 107, Appl
33	447	79.4	107	16	US-10-462-062-182	Sequence 182, App
34	447	79.4	127	15	US-10-472-905A-96	Sequence 96, Appl
35	447	79.4	127	16	US-10-462-062-182	Sequence 182, App
36	447	79.4	127	15	US-10-472-905A-122	Sequence 122, App
37	443	78.7	109	10	US-09-802-083-3	Sequence 3, Appli
38	443	78.7	109	14	US-09-165-732A-3	Sequence 3, Appli
39	443	78.7	109	14	US-10-172-785-3	Sequence 3, Appli
40	441	78.3	107	15	US-10-745-455-3	Sequence 3, Appli
41	439	78.0	107	16	US-10-412-406-4	Sequence 4, Appli
42	439	78.0	663	15	US-10-412-406-32	Sequence 32, Appl
43	436	77.4	107	15	US-10-462-062-101	Sequence 101, App
44	436	77.4	107	16	US-10-472-905A-90	Sequence 90, Appl
45	436	77.4	127	15	US-10-462-062-181	Sequence 181, App

ALIGNMENTS

RESULT 1
US-10-774-076-3

; Sequence 3, Application US/10774076
; Publication No. US20040210004A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Landolfi, et al.
TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
TITLE OF INVENTION: Psoriasis
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2

SEQ ID NO 3
LENGTH: 107
TYPE: PRT
ORGANISM: mus sp.
US-10-774-076-3

Query Match   100.0%; Score 563; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 6e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
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Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPFYTFGGGTKLEIK 107
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEPFYTFGGGTKLEIK 107

RESULT 2
US-10-774-076-11
; Sequence 11, Application US/10774076

; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-11

Query Match   100.0%; Score 563; DB 17; Length 127;
Best Local Similarity   100.0%; Pred. No. 7.2e-42;
Matches 107; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFPYTFGGGTKLEIK 107
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFPYTFGGGTKLEIK 127

RESULT 3
US-10-436-782-33
; Sequence 33, Application US/10436782
; Publication No. US20040028685A1
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; APPLICANT: Kiener, Peter
; APPLICANT: Langermann, Solomon
; TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof
; FILE REFERENCE: 10271-097
; CURRENT APPLICATION NUMBER: US/10/436,782
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,322
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/418,213
; PRIOR FILING DATE: 2002-10-14
; PRIOR APPLICATION NUMBER: 60/418,213
; PRIOR FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-436-782-33

Query Match   98.8%; Score 556; DB 15; Length 107;
Best Local Similarity   98.1%; Pred. No. 2.5e-41;
Matches 105; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLKYDEFPYTFGGGTKLEIK 107
              ||||||||||||||||||||||||||||||||||||:|||||||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLKYDEFPYTFGGGTKLEIK 107

RESULT 4
US-10-436-783-1
; Sequence 1, Application US/1043678

; Publication No. US20040091486A1
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael
; APPLICANT: Carles-Kinch, Kelly
; TITLE OF INVENTION: EphA2 Agonistic Monoclonal Antibodies and Methods of Use Thereof
; FILE REFERENCE: 10271-107
; CURRENT APPLICATION NUMBER: US/10/436,783
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,368
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/418,204
; PRIOR FILING DATE: 2002-10-14
; PRIOR APPLICATION NUMBER: 60/460,358
; PRIOR FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-436-783-1

Query Match   98.8%; Score 556; DB 15; Length 107;
Best Local Similarity   98.1%; Pred. No. 2.5e-41;
Matches 105; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLKYDEFPYTFGGGTKLEIK 107
              ||||||||||||||||||||||||||||||||||||:|||||||||||
Db   61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLKYDEFPYTFGGGTKLEIK 107

RESULT 5
US-10-340-189-26
; Sequence 26, Application US/10340189
; Publication No. US20030229207A1
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 W. Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/340,189
; FILING DATE: 10-Jan-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,202A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-340-189-26

Query Match
Best Local Similarity   96.1%;   Score 541;   DB 14;   Length 107;
Matches 103;   Conservative   2;   Pred. No. 5.1e-40;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
       ||||||||||||||||||:||||||||| :|:||:|:||||||||||
Db 61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 6
US-10-325-696-26:
Sequence 26, Application US/10325696
Publication No. US20040005630A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
NUMBER OF SEQUENCES: 67
TITLE OF INVENTION: Modified Antibody Variable Domains
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11103US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-325-696-26

Query Match
Best Local Similarity   96.1%;   Score 541;   DB 15;   Length 107;
Matches 103;   Conservative   2;   Pred. No. 5.1e-40;   Mismatches   2;   Indels   0;   Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK 107
       ||||||||||||||||||:||||||||| :|:||:|:||||||||||
Db 61 RFSGSGSGQDYSLTISSLDYEDMGIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 7
US-10-127-890-123:
Sequence 123, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
          Carroll, Stephen F.
          Studnika, Gary M.
NUMBER OF SEQUENCES: 173
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-10-127-890-123

Query Match   94.3%;   Score 531;   DB 14;   Length 107;

RESULT 8
US-09-158-120A-21
Sequence 21, Application US/09158120A
Patent No. US20010022257A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
;   Respiratory Syncytial Virus
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;   STEWART & OLSTEIN
;   STREET: 6 BECKER FARM ROAD
;   CITY: ROSELAND
;   STATE: NEW JERSEY
;   COUNTRY: USA
;   ZIP: 07068
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 INCH DISKETTE
;   COMPUTER: P160
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: MS Word 97
; CURRENT APPLICATION DATA:
;   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;   APPLICATION NUMBER: US/09/158,120A
;   FILING DATE: September 21, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/290,592
;   FILING DATE: August 15, 1994
;   APPLICATION NUMBER: 07/813,372
;   FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Olstein, Elliot M.
;   REGISTRATION NUMBER: 24,025
;   REFERENCE/DOCKET NUMBER: 469201-367
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 973-994-1700
;   TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 107 AMINO ACIDS
;   TYPE: AMINO ACID
;   TOPOLOGY: LINEAR
;   MOLECULE TYPE: PROTEIN

Query Match   93.8%;   Score 527; DB 9;   Length 107;
Best Local Similarity   92.5%;   Pred. No. 8.7e-39;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
           |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINRYLNWFQQKPGKSPKTLIHRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDFPYTFGGGTKLEIK 107
           ||||||||||||||||||||||||||:|||||||||||||||||||
Db   61 RFSGSGSGQEYSLTISSLEFEDMGIYYCLQFHFPYTFGGGTKLEIK 107

; Sequence 2, Application US/09797481
; Patent No. US20010047083A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
;   Kohler, Heinz
;   Foon, Kenneth A.
;   Chatterjee, Sunil K.
; TITLE OF INVENTION: MURINE ANTI-IDIOTYPE ANTIBODY 3H1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: MORRISON & FOERSTER
;   STREET: 755 Page Mill Road
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304-1018
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/797,481
;   FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 09/361,772
;   FILING DATE: 27-JUL-1999
;   APPLICATION NUMBER: US 08/579,940
;   FILING DATE: 28-DEC-1995
;   APPLICATION NUMBER: US 08/365,484
;   FILING DATE: 28-DEC-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: CATHERINE M. POLIZZI
;   REGISTRATION NUMBER: 40,130
;   REFERENCE/DOCKET NUMBER: 304142000102
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 813-5600
;   TELEFAX: (650) 494-0792
;   TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 142 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-797-481-2

Query Match   92.7%;   Score 522; DB 9;   Length 142;
Best Local Similarity   91.6%;   Pred. No. 3.2e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
           |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   21 DIKMTQSPSSMYASLGERVTITCKASQDINGYLNWFQQEPGKSPKTLIYRANRLVDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDFPYTFGGGTKLEIK 107
           |||||||||||||||||||||||||||:|||:||||::|||||||||
Db   81 RFSGSGSGQVYSLTISSLEYEDMGTYYCLQFDFPWMFGGGTKLEIK 127

RESULT 10
US-09-844-736-4
Sequence 4, Application US/09844736
Patent No. US20020041872A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
;   Foon, Kenneth A.
;   Chatterjee, Sunil K.
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
;   CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
; NUMBER OF SEQUENCES: 6

Best Local Similarity   94.4%;   Pred. No. 3.9e-39;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFHHKPGKSPKTLIYRANRLVDGVPS 60

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDFPYTFGGGTKLEIK 107
           ||||||||||||||||||||||||||||||:|||||||||||||||
Db   61 RFSGSGSGQDYSLTISSLDYEDMGITYYCQQYDESPWTFGGGTKLEIK 107

RESULT 11
US-10-162-396-4
Sequence 4, Application US/10162396
; Publication No. US20030077274A1
; GENERAL INFORMATION:
;   APPLICANT: Chatterjee, Malaya
;   Foon, Kenneth A.
;   Chatterjee, Sunil K.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
                    CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
   ADDRESSEE: MORRISON & FOERSTER
   STREET: 755 PAGE MILL ROAD
   CITY: PALO ALTO
   STATE: CA
   COUNTRY: USA
   ZIP: 94304-1018
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/10,162,396
   FILING DATE: 06-Apr-2004
   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 10/162,396
   FILING DATE: June 3, 2002
   APPLICATION NUMBER: US 09/844,736

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
   LENGTH: 142 amino acids
   TYPE: amino acid
   STRANDEDNESS: single
   TOPOLOGY: linear
   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-162-396-4

Query Match   92.7%; Score 522; DB 14; Length 142;
Best Local Similarity   91.6%; Pred. No. 3.2e-38;
Matches 98; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy   1 DIKWTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db   21 DIKWTQSPSSMYASLGERVTITCKASQDINGYLNWFQQEPGKSPKTLIYRANRLIDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDBFPYTFGGGTKLEIK 107
           |||||||| ||||||||||||||:||||:||| |:|||||||||||
Db   81 RFSGSGSGQVYSLTISSLEYEDMGTYYCLQFDBFPWMFGGGTKLEIK 127

RESULT 12
US-10-819-493-4
Sequence 4, Application US/10819493
; Publication No. US20040253230A1
; GENERAL INFORMATION:
;   APPLICANT: Chatterjee, Malaya
;   Foon, Kenneth A.
;   Chatterjee, Sunil K.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
                    CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
   ADDRESSEE: MORRISON & FOERSTER
   STREET: 755 PAGE MILL ROAD
   CITY: PALO ALTO
   STATE: CA
   COUNTRY: USA
   ZIP: 94304-1018
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/10/819,493
   FILING DATE: April 12, 1996
   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 09/844,736
   FILING DATE: April 9, 1997
   APPLICATION NUMBER: US 08/838,692
   FILING DATE: April 27, 2001
   APPLICATION NUMBER: US 60/044,455
   FILING DATE: April 9, 1997
   APPLICATION NUMBER: US 08/631,085
   FILING DATE: April 12, 1996

ATTORNEY/AGENT INFORMATION:
   NAME: Polizzi, Catherine M.
   REGISTRATION NUMBER: 40,130
   REFERENCE/DOCKET NUMBER: 30414200000402
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (415) 813-5600
   TELEFAX: (415) 494-0792
   TELEX: 706141

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
   LENGTH: 142 amino acids
   TYPE: amino acid
   STRANDEDNESS: single
   TOPOLOGY: linear
   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-162-396-4

Query Match   92.7%; Score 522; DB 14; Length 142;
Best Local Similarity   91.6%; Pred. No. 3.2e-38;
Matches 98; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy   1 DIKWTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db   21 DIKWTQSPSSMYASLGERVTITCKASQDINGYLNWFQQEPGKSPKTLIYRANRLIDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDBFPYTFGGGTKLEIK 107
           |||||||| ||||||||||||||:||||:||| |:|||||||||||
Db   81 RFSGSGSGQVYSLTISSLEYEDMGTYYCLQFDBFPWMFGGGTKLEIK 127

APPLICATION NUMBER: US/10/162,396
FILING DATE: 31-Jul-2002
CLASSIFICATION: <Unknown>

CORRESPONDENCE ADDRESS:
   ADDRESSEE: MORRISON & FOERSTER
   STREET: 755 PAGE MILL ROAD
   CITY: PALO ALTO
   STATE: CA
   COUNTRY: USA
   ZIP: 94304-1018
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/09/844,736
   FILING DATE: 09-Apr-1997
   CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: 08/838,692
   FILING DATE: April 9, 1997
ATTORNEY/AGENT INFORMATION:
   NAME: Polizzi, Catherine M.
   REGISTRATION NUMBER: 40,130
   REFERENCE/DOCKET NUMBER: 30414-20004.01
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (415) 813-5600
   TELEFAX: (415) 494-0792
   TELEX: 706141

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
   LENGTH: 142 amino acids
   TYPE: amino acid
   STRANDEDNESS: single
   TOPOLOGY: linear
   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-844-736-4

Query Match   92.7%; Score 522; DB 9; Length 142;
Best Local Similarity   91.6%; Pred. No. 3.2e-38;
Matches 98; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy   1 DIKWTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db   21 DIKWTQSPSSMYASLGERVTITCKASQDINGYLNWFQQEPGKSPKTLIYRANRLIDGVPS 80

Qy   61 RFSGSGSGQDYSLTISSLEYEDMGIIYCLQYDBFPYTFGGGTKLEIK 107
           |||||||| ||||||||||||||:||||:||| |:|||||||||||
Db   81 RFSGSGSGQVYSLTISSLEYEDMGTYYCLQFDBFPWMFGGGTKLEIK 127

FILING DATE: April 27, 2001
APPLICATION NUMBER: US 08/838,692
FILING DATE: April 9, 1997
APPLICATION NUMBER: US 60/044,455
FILING DATE: April 12, 1996
APPLICATION NUMBER: US 08/631,085
FILING DATE: April 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jacobson, Jill
REGISTRATION NUMBER: 40,030
REFERENCE/DOCKET NUMBER: 30414200000403
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-819-493-4

Query Match   92.7%; Score 522; DB 17; Length 142;
Best Local Similarity   91.6%; Pred. No. 3.2e-38;
Matches   98; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        |||||||||||||||||||||||||||||||:||:||||:|||||||||||||||:||||
Db 21 DIKMTQSPSSMYASLGERVTITCKASQDINGYLNWFQQEPGKSPKTLIYRANRLIDGVPS 80

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFPYTFGGGTKLEIK 107
        |||||||||:||||||||||||||:|||||||:||||||:||||||||
Db 81 RFSGSGSGQVYSLTISSLEYEDMGTYYYCLQFDEFPWMFGGGTKLEIK 127

RESULT 13
US-10-340-189-27
Sequence 27, Application US/10340189
Publication No. US20030229207A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-10-340-189-27

Query Match   90.2%; Score 508; DB 14; Length 107;
Best Local Similarity   89.7%; Pred. No. 4e-37;
Matches   96; Conservative   6; Mismatches   5; Indels   0; Gaps   0;

Qy   1 DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
        ||:|||||||||:|||||:|||||:||||||||||||||||||||||||||||||||||
Db   1 DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy 61 RFSGSGSGQDYSLTISSLEYEDMGIIYYCLQYDEFPYTFGGGTKLEIK 107
        ||||||||:|:|:||||:|||||:|||||||:|||||:||||||||||
Db 61 RFSGSGSGQTDYLTITSSLQYEDFGIIYYCQQYDESPWTFGGGTKLEIK 107

RESULT 14
US-10-325-696-27
Sequence 27, Application US/10325696
Publication No. US20040005630A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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;
US-10-325-696-27
    SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Query Match      90.2%;   Score 508;   DB 15;   Length 107;
Best Local Similarity   89.7%;   Pred. No. 4e-37;
Matches   96;   Conservative   6;   Mismatches   5;   Indels   0;   Gaps   0;

Qy   1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60
        ||:|||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db   1  DIQMTQSPSSMSASLGDRVTITCRASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60

Qy  61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK  107
        |||:||||||||||:|||||:|||  ||||  |:||||||||||||:|||
Db  61  RFSGSGSGTDYTLTISSLQYEDFPGIYYCQQYDESPWTFGGGTKLEIK  107

RESULT 15
US-10-774-076-14
;  Sequence 14, Application US/10774076
;  Publication No. US20040210040A1
;  GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs, Inc.
;  APPLICANT: Landolfi, et al.
;  TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
;  TITLE OF INVENTION: Psoriasis
;  FILE REFERENCE: 05882.0064.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/774,076
;  CURRENT FILING DATE: 2004-02-06
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: Patentin version 3.2
;
;  SEQ ID NO 14
;  LENGTH: 107
;  TYPE: PRT
;  ORGANISM: Artificial
;  FEATURE:
;  OTHER INFORMATION: Humanized antibody
US-10-774-076-14

Query Match      89.3%;   Score 503;   DB 17;   Length 107;
Best Local Similarity   87.9%;   Pred. No. 1.1e-36;
Matches   94;   Conservative   8;   Mismatches   5;   Indels   0;   Gaps   0;

Qy   1  DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS  60
        ||:|||||||||||||||||||||:|||||||||||||||||:|||||||||||||||||
Db   1  DIQMTQSPSSLSASVGDRVTITCKASQDINSYLSWFQQKPGKAPKTLIYRANRLVDGVPS  60

Qy  61  RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIK  107
        ||||||||||||:||||||:||  ||  |||||||||||||||:||||
Db  61  RFSGSGSGQDYTLTISSLQPEDFATYYCLQYDEFPYTFGGGTKVEIK  107
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Search completed: December 29, 2004, 18:41:57
Job time : 64.8643 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 29, 2004, 18:05:34

Title: US-10-774-076-2
Perfect score: 648
Sequence: 1 EIQLQQSGPELVKPGASVKV........GNPPYYFDYWGQGTTLTVSS 119

Scoring table: BLOSUM62
                     Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Post-processing: Minimum Match 100%
                     Maximum Match 100%
                     Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US0A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US0B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	648	100.0	119	17	US-10-774-076-2	Sequence 2, Appli
2	648	100.0	138	17	US-10-774-076-9	Sequence 9, Appli
3	564	87.0	119	17	US-10-642-122-2	Sequence 2, Appli
4	564	87.0	138	17	US-10-774-076-12	Sequence 12, Appl
5	560.5	86.5	138	17	US-10-774-076-17	Sequence 17, App
6	560.5	86.5	118	15	US-10-462-062-139	Sequence 139, App
7	560.5	86.5	118	15	US-10-462-062-140	Sequence 140, App
8	560.5	86.5	137	15	US-10-462-062-153	Sequence 153, App
9	548.5	84.6	137	15	US-10-462-062-154	Sequence 154, App
10	529	81.6	120	15	US-10-372-719-2	Sequence 2, Appli
11	523.5	80.8	117	14	US-10-223-880-2	Sequence 2, Appl
12	517	79.8	139	15	US-10-365-123-28	Sequence 28, Appl
13	517	79.8	117	15	US-10-383-447-14	Sequence 14, Appl
14	514.5	79.4	152	16	US-10-642-120-2	Sequence 2, Appli
15	514.5	79.4	152	16	US-10-642-060-2	Sequence 2, Appli
16	514.5	79.4	152	16	US-10-642-122-2	Sequence 2, Appli
17	514.5	79.4	152	16	US-10-642-124-2	Sequence 2, Appl
18	514.5	79.4	152	16	US-10-521-269-2	Sequence 2, Appli
19	514.5	79.4	152	16	US-10-620-850-2	Sequence 2, Appli
20	514.5	79.4	152	17	US-10-642-118-2	Sequence 2, Appli
21	514.5	79.4	152	17	US-10-642-117-2	Sequence 2, Appli
22	514.5	79.4	152	17	US-10-642-119-2	Sequence 2, Appli
23	512.5	79.1	152	17	US-10-642-099-2	Sequence 2, Appli
24	512.5	79.1	118	15	US-10-462-062-144	Sequence 144, App
25	512.5	79.1	137	15	US-10-462-062-158	Sequence 158, App
26	503.5	77.7	116	15	US-09-940-727B-90	Sequence 90, Appl
27	503.5	77.7	118	15	US-10-462-062-143	Sequence 143, App
28	503.5	77.7	137	15	US-10-462-062-157	Sequence 157, App
29	502	77.5	119	15	US-09-215-163-44	Sequence 44, Appl
30	498.5	76.9	116	10	US-09-940-727B-14	Sequence 14, Appl
31	496	76.5	117	10	US-09-990-586-4	Sequence 4, Appli
32	496	76.5	117	14	US-10-310-113-4	Sequence 4, Appli
33	496	76.5	117	14	US-10-230-880-4	Sequence 4, Appli
34	494	76.2	136	16	US-10-768-193-7	Sequence 7, Appli
35	492	75.9	117	9	US-09-293-854-4	Sequence 4, Appli
36	492	75.9	117	14	US-09-293-417-4	Sequence 4, Appli
37	492	75.9	117	17	US-10-764-140-4	Sequence 4, Appli
38	490.5	75.7	116	14	US-10-389-155-15	Sequence 15, Appl
39	490.5	75.7	116	15	US-10-389-155-15	Sequence 15, Appl
40	490.5	75.7	116	15	US-10-452-357-56	Sequence 56, Appl
41	490.5	75.7	116	15	US-10-452-357-56	Sequence 56, Appl
42	490.5	75.7	135	14	US-10-389-155-60	Sequence 60, Appl
43	490.5	75.7	135	15	US-10-389-155-60	Sequence 60, Appl
44	490	75.6	117	15	US-10-452-357-69	Sequence 69, Appli
45	490	75.6	117	17	US-10-816-938-10	Sequence 10, Appl
46	490	75.6	130	9	US-09-839-447A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-774-076-2
; Sequence 2, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-2

Query Match   100.0%; Score 648; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-52;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYMYMWVKQSHGKSLEWIGYIDPYYGDPGY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYMYMWVKQSHGKSLEWIGYIDPYYGDPGY 60

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVSS 119
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVSS 119

RESULT 2
US-10-774-076-9
; Sequence 9, Application US/10774076

; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 9
; LENGTH: 138
; TYPE: PRT
; ORGANISM: mus sp.

US-10-774-076-9

Query Match   100.0%;
Best Local Similarity   100.0%;
Matches 119;   Conservative   0;

Qy   1   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 20   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 79

Qy 61   SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPYYFDYWGQGTTLTVSS 119
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 80   SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPYYFDYWGQGTTLTVSS 138

RESULT 3
US-10-774-076-12
; Sequence 12, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody

US-10-774-076-12

Query Match   87.0%;   Score 564;   DB 17;   Length 119;
Best Local Similarity   84.9%;   Pred. No. 1.6e-44;
Matches 101;   Conservative   9;   Mismatches   9;   Indels   0;   Gaps   0;

Qy   1   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |:||| |||||||||||||||:|||||||||||||||||||||||||||||||||||:||||
Db   1   EVQLVQSGAEVKKPGASVKISCKVSGYAFTNYNIMYWVRQAPGKGLEWIGYIDPYYGDPGY 60

Qy 61   SQKFKGKATLTVDKSSTAYMHLNSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
          |||||| |||||:|||| |:||| |||||||||||||||||||||||||||||||||
Db 61   SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARGNFPYYFDYWGQGTTLVTVSS 119

RESULT 4
US-10-774-076-17
; Sequence 17, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and

---

; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 17
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody

US-10-774-076-17

Query Match   87.0%;   Score 564;   DB 17;   Length 138;
Best Local Similarity   84.9%;   Pred. No. 1.8e-44;
Matches 101;   Conservative   9;   Mismatches   9;   Indels   0;   Gaps   0;

Qy   1   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 20   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 79

Qy 61   SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPYYFDYWGQGTTLTVSS 119
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 80   SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPYYFDYWGQGTTLTVSS 138

RESULT 5
US-10-462-062-139
; Sequence 139, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 139
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
; OTHER INFORMATION: H chain V region of anti TF mouse monoclonal antibody ATR-2

US-10-462-062-139

Query Match   87.0%;   Score 564;   DB 17;   Length 138;
Best Local Similarity   84.9%;   Pred. No. 1.8e-44;
Matches 101;   Conservative   9;   Mismatches   9;   Indels   0;   Gaps   0;

Qy   1   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 20   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 79

Qy 61   SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
          ||||||||||||||||:|||||| ||:||| |||||||||||||||||||||||||||||
Db 80   SQKFKGKATLTVDKSTSTAYMELSSLRSEDTAVYYCARRGNFPYYFDYWGQGTTLVTVSS 138

RESULT 6
US-10-462-062-140
; Sequence 140, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH

Query Match   86.5%;   Score 560.5;   DB 15;   Length 118;
Best Local Similarity   89.9%;   Pred. No. 3.3e-44;
Matches 107;   Conservative   4;   Mismatches   7;   Indels   1;   Gaps   1;

Qy   1   EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNIMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |||||||||||||||||||||||||:|||:||||||||||||||||||||||||||||||
Db   1   EIQLQQSGPELVKPGASVKVSCKASGYSFDYNMMYWVRQAPGKGLEWIGYIDPYYGNGGTIY 60

Qy 61   SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
          :||||||||||||||||:|||||||||||| |||||| ||||||||||||||||||||||
Db 61   NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLVTVSS 118

```
RESULT 7
US-10-462-062-153
  Sequence 153, Application US/10462062
  Publication No. US20040041187A1
; GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: ADACHI, HIDEKI
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;  TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;  FILE REFERENCE: 053466-0360
;  CURRENT APPLICATION NUMBER: US/10/462,062
;  CURRENT FILING DATE: 2003-06-16
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 153
;  LENGTH: 137
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
;  OTHER INFORMATION: sequence for H chain v region of anti-TF mouse monoclonal
;  OTHER INFORMATION: antibody ATR-2
US-10-462-062-153

Query Match             86.5%;  Score 560.5;  DB 15;  Length 137;
Best Local Similarity   89.9%;  Pred. No. 3.9e-44;
Matches  107;  Conservative   4;  Mismatches   7;  Indels   1;  Gaps   1;

Qy      1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60

Qy     61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYPDYWGQGTTLTVSS 119
          ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db     61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLTVSS 118
```

```
RESULT 8
US-10-462-062-154
  Sequence 154, Application US/10462062
  Publication No. US20040041187A1
; GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT: ADACHI, HIDEKI
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;  TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;  FILE REFERENCE: 053466-0360
;  CURRENT APPLICATION NUMBER: US/10/462,062
;  CURRENT FILING DATE: 2003-06-16
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 154
;  LENGTH: 137
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
;  OTHER INFORMATION: sequence for H chain v region of anti-TF mouse monoclonal
;  OTHER INFORMATION: antibody ATR-3
US-10-462-062-154

Query Match             86.5%;  Score 560.5;  DB 15;  Length 137;
Best Local Similarity   89.9%;  Pred. No. 3.9e-44;
Matches  107;  Conservative   4;  Mismatches   7;  Indels   1;  Gaps   1;

Qy      1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     20 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 79

Qy     61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYPDYWGQGTTLTVSS 119
          ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db     80 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLTVSS 137
```

```
RESULT 9
US-10-372-719-2
  Sequence 2, Application US/10372719
  Publication No. US20040005643A1
; GENERAL INFORMATION:
;  APPLICANT: DE SANTIS, RITA
;  APPLICANT: ANASTASI, ANNA MARIA
;  TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY
;  FILE REFERENCE: 2818-141
;  CURRENT APPLICATION NUMBER: US/10/372,719
;  CURRENT FILING DATE: 2003-02-25
;  PRIOR APPLICATION NUMBER: 60/359,299
;  PRIOR FILING DATE: 2002-02-26
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
;  LENGTH: 120
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;  OTHER INFORMATION: ST2146 heavy chain variable region protein sequence
US-10-372-719-2

Query Match             84.6%;  Score 548.5;  DB 15;  Length 120;
Best Local Similarity   86.7%;  Pred. No. 4.3e-43;
Matches  104;  Conservative   6;  Mismatches   9;  Indels   1;  Gaps   1;

Qy      1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          ::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    1 KVKLQQSGPELVKPGASVKVSCKASGYAFTSYNMYWVKQSHGKSLEWIGYIDPYNGVTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYY-FDYWGQGTTLTVSS 119
         :||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGGGSIYYAMDYWGQGTTVVSS 120
```

RESULT 10
US-10-223-880-2
; Sequence 2, Application US/10223880
; Publication No. US20030152571A1
; GENERAL INFORMATION:
;   APPLICANT: JOHANSON, KYUNG O.
;   APPLICANT: JONAK, ZDENKA
;   APPLICANT: TAYLOR, ALEXANDER
;   TITLE OF INVENTION: ANTI-ALPHABETA3 HUMANIZED MONOCLONAL
;   TITLE OF INVENTION: ANTIBODIES
;   FILE REFERENCE: P50629C1
;   CURRENT APPLICATION NUMBER: US/10/223,880
;   CURRENT FILING DATE: 2002-08-20
;   PRIOR APPLICATION NUMBER: 09/380,910
;   PRIOR FILING DATE: 1999-09-10
;   PRIOR APPLICATION NUMBER: PCT/US98/04987
;   PRIOR FILING DATE: 1998-03-12
;   PRIOR APPLICATION NUMBER: 60/039,609
;   PRIOR FILING DATE: 1997-03-12
;   NUMBER OF SEQ ID NOS: 45
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 2
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Mus musculus

Query Match   81.6%; Score 529; DB 14; Length 117;
Best Local Similarity   84.3%; Pred. No. 2.7e-41;
  Matches 102; Conservative 8; Mismatches 5; Indels 6; Gaps 2;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYNGDTFY 60
          |:||||||||||||||||||||||||||:|||||||||||||||||||||
Db   1 EIQLQQSGPEVVKPGASVKVSCKASGYAFTSYNMYWVKQSHGKSLEWIGYIDPYNGDTFY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARR--GNFPYYFDYWGQGTTLTVS 118
          :||||||||||||||||||||||||||||||||| ||||||||||||:|||
Db   61 NQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVFYCARQNYGSFA----YWGQGTTLVTVS 116
```

RESULT 11
US-10-365-123-28
; Sequence 28, Application US/10365123
; Publication No. US20040053365A1
; GENERAL INFORMATION:
;   APPLICANT: Renner, Christoph
;   APPLICANT: Scott, Andrew
;   APPLICANT: Burgess, Antony
;   TITLE OF INVENTION: HUMANIZED GM-CSF ANTIBODIES
;   FILE REFERENCE: LUD 5729.1
;   CURRENT APPLICATION NUMBER: US/10/365,123
;   CURRENT FILING DATE: 2003-02-12
;   NUMBER OF SEQ ID NOS: 56
;
;   SEQ ID NO 28
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region

Query Match   80.8%; Score 523.5; DB 15; Length 139;

Best Local Similarity   81.5%; Pred. No. 1e-40;
  Matches 97; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

```
Qy    1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          :|||||||||||||||||:|||||:|| :||||||||||:||||||:||  ||:||
Db   18 EVQLQQSGPELVKPGASVKISCKASGYTFTDYNIIHWVKQSHGKSLDWIGYIAPYSGGTGY 77

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
          :|| |:|||||||||||||||| :|||:||||||||||||  ||:||||||||||||
Db   78 NQBFKNRATLTVDKSSSTAYMBLRSLTSDDSAVYYCARDRFP-YFDYWGQGTLRVSS 135
```

RESULT 12
US-10-383-447-14
; Sequence 14, Application US/10383447
; Publication No. US20040096339A1
; GENERAL INFORMATION:
;   APPLICANT: Bhaskar, Vinay
;   APPLICANT: de la Calle, Agustin
;   APPLICANT: Law, Debbie
;   APPLICANT: Caras, Ingrid
;   APPLICANT: Ramakrishnan, Vanitha
;   APPLICANT: Murray, Richard
;   APPLICANT: Afar, Daniel
;   APPLICANT: Powers, David
;   TITLE OF INVENTION: Antibodies Against Cancer Antigen TMEFF2 and Uses Thereof
;   FILE REFERENCE: 05882.0138.NPUS00
;   CURRENT APPLICATION NUMBER: US/10/383,447
;   CURRENT FILING DATE: 2002-03-07
;   PRIOR APPLICATION NUMBER: US 60/362,837
;   PRIOR FILING DATE: 2002-03-08
;   PRIOR APPLICATION NUMBER: US 60/463,812
;   PRIOR FILING DATE: 2002-12-27
;   NUMBER OF SEQ ID NOS: 34
;   SOFTWARE: Patentin version 3.2
;
;   SEQ ID NO 14
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Heavy chain variable region

Query Match   79.8%; Score 517; DB 15; Length 117;
Best Local Similarity   82.4%; Pred. No. 3.4e-40;
  Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 1;

```
Qy    1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |||||||||||:||||||:|:||||:|| :|  :||||||||: |||||||||: |:||
Db    1 EIQLQQSGPELMKPGASVKRISCKASTYSFTRYFMHWVKQSHGHESLEWIGYIDPFNGGTGY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
          :|||||||||||||||||||| :|||||||||||  ||  ||:||||||||||:|||
Db   61 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCVTYGS--DYFDYWGQGTTLRVSS 117
```

RESULT 13
US-10-769-612-3
; Sequence 3, Application US/10769612
; Publication No. US20040141983A1
; GENERAL INFORMATION:
;   APPLICANT: Law, Debbie
;   APPLICANT: Gish, Kurt C.
;   APPLICANT: Murray, Richard
;   APPLICANT: Culp, Patricia
;   TITLE OF INVENTION: Compositions Against Cancer Antigen LIV-1 And Uses Thereof
;   FILE REFERENCE: 05882.0129.CPUS08
;   CURRENT APPLICATION NUMBER: US/10/769,612
;   CURRENT FILING DATE: 2004-01-29
;   PRIOR APPLICATION NUMBER: 60/443,712
;   PRIOR FILING DATE: 2003-01-29
;   PRIOR APPLICATION NUMBER: 09/642,034
;   PRIOR FILING DATE: 2000-08-18

```
;  PRIOR APPLICATION NUMBER: 09/525,361
;  PRIOR FILING DATE: 2000-03-15
;  PRIOR APPLICATION NUMBER: 09/453,137
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: 09/450,810
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: 09/268,865
;  PRIOR FILING DATE: 1999-03-15
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: Patentin version 3.2
;
;  SEQ ID NO 3
;  LENGTH: 117
;  TYPE: PRT
;  ORGANISM: Mus musculus
US-10-769-612-3

RESULT 14
US-10-642-120-2
;  Sequence 2, Application US/10642120
;  Publication No. US20040131610A1
;  GENERAL INFORMATION:

Query Match             79.8%;  Score 517;  DB 16;  Length 117;
Best Local Similarity   82.4%;  Pred. No. 3.4e-40;
Matches  98;  Conservative   9;  Mismatches 10;  Indels   2;  Gaps   1;

Qy   1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        :||||||||||||:||||||||||:|| ||| ||||||||||||||||:|||||||||
Db   1  EIQLQQSGPELMKPGASVKISCKASTYSFTRYFMHWVKQSHGBSLEWIGYIDPFNGGTGY 60

Qy  61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
        :|||||||||||||||||||:||| ||||||||||||    ||:  ||||||||||||||
Db  61  NQKFRGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCVTYGS--DYFDYWGQGTTLTVSS 117

RESULT 15
US-10-642-060-2
;  Sequence 2, Application US/10642060
;  Publication No. US20040131621A1
;  GENERAL INFORMATION:
;  APPLICANT: Thorpe, Philip E.
;  APPLICANT: Soares, M. Melina
;  APPLICANT: Ran, Sophia
;  TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using Antibo
;  TITLE OF INVENTION: Aminophospholipids
;  FILE REFERENCE: 4001.002982
;  CURRENT APPLICATION NUMBER: US/10/642,060
;  CURRENT FILING DATE: 2003-08-15
;  PRIOR APPLICATION NUMBER: US 10/621,269
;  PRIOR FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: 60/396,263
;  PRIOR FILING DATE: 2002-07-15
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: Patentin version 3.1
;
;  SEQ ID NO 2
;  LENGTH: 152
;  TYPE: PRT
;  ORGANISM: Mus musculus
US-10-642-060-2

Query Match             79.4%;  Score 514.5;  DB 16;  Length 152;
Best Local Similarity   80.0%;  Pred. No. 7.7e-40;
Matches  96;  Conservative  10;  Mismatches 13;  Indels   1;  Gaps   1;

Qy   1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        :|||||||||| |||||||:||||||:|| ||| ||||||||||||||||:|||||||||
Db  20  EVQLQQSGPELEKPGASVKLSCKASGYSFTGYNMNWVKQSHGKSLEWIGHIDPYYGDTSY 79

Qy  61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNP-PYYFDYWGQGTTLTVSS 119
        :|||||||||||||||||||  : :|||||||||||  ||:  ||||||||||||||||||
Db  80  NQKFRGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCVKGGYYGHWYFDVWGAGTTVTVSS 139

Search completed: December 29, 2004, 18:41:54
Job time : 74.8024 secs
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OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 ; Search time 81.7906 Seconds
(without alignments)
521.928 Million cell updates/sec

Title:
Perfect Score: 648
Sequence: 1 EIQLQQSGPELVKPGASVKV..........GNFPYYFDYWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	560.5	86.5	118	2	AAY52755 Anti-tiss
2	560.5	86.5	118	2	AAY52756 Anti-tiss
3	548.5	84.6	120	7	ABR82930 Anti-huma
4	541	83.5	140	7	ADC24943 Mouse 19/
5	541	83.5	140	7	ADK51711 Murine 19
6	529	81.7	116	2	AAW95481 Mouse der
7	529	81.6	117	2	AAW84093 Murine vi
8	525.5	81.1	214	6	ABP96759 TSH recep
9	525.5	81.1	214	6	ABP96760 TSH recep
10	525.5	81.1	214	6	ABP96763 TSH recep
11	520.5	80.3	214	6	ABP96764 TSH recep
12	518.5	80.0	239	7	ADC79231 Anti-CA12
13	517	79.8	117	7	ADC27445 TMBFP2#20
14	516.5	79.7	214	6	ABP96756 TSH recep
15	516.5	79.7	214	6	ABP96755 TSH recep
16	514.5	79.4	152	8	ADJ57084 3G4 antib
17	514.5	79.4	159	8	ADJ57088 3G4-2BVH-
18	512.5	79.1	118	2	AAY52760 Anti-tiss
19	512	79.0	112	5	AAE15811 Human mAb
20	507.5	78.3	239	7	ADC79232 Control s
21	506.5	78.2	135	2	AAR28669 p12-h2. 3
22	505	77.9	267	3	AAB09776 TMV 30K m
23	504.5	77.9	116	3	AAW71882 Anti-Fas
24	504.5	77.9	116	3	AAB12919 Anti-huma
25	504.5	77.9	130	2	AAW71886 Anti-Fas
26	504.5	77.9	135	2	AAW60866 Variable
27	504.5	77.9	135	3	AAY80293 IgM chime
28	504.5	77.9	467	6	AAE38408 Mouse vir
29	504.5	77.9	590	2	AAW31751 H chain s
30	504.5	77.9	590	2	AAW71888 Anti-huma
31	504.5	77.9	590	3	AAB12908 Anti-huma
32	503.5	77.7	116	2	AAW39889 Heavy cha
33	503.5	77.7	118	2	AAY52759 Anti-tiss
34	502.5	77.5	116	2	AAW60864 Variable
35	502	77.5	119	2	AAY21819 11810 ant
36	501.5	77.4	120	8	ADI26469 Murine I4
37	501.5	77.4	162	2	AAW01752 MHI monoc
38	501.5	77.1	137	2	AAR05090 Heavy cha
39	498.5	76.9	116	2	AAW39810 Variable
40	497.5	76.8	263	2	AAW90226 Anti-B7.2
41	497.5	76.8	268	2	AAW90222 Anti-B7.2
42	497.5	76.8	580	2	AAW90217 Bispecifi
43	496	76.5	117	2	AAW71288 Human ant
44	496	76.5	117	6	ABR42700 Anti-tiss
45	496	76.5	117	6	ABR42718 Anti-tiss

ALIGNMENTS

RESULT 1
AAY52755
ID AAY52755 standard; protein; 118 AA.
AC AAY52755;
DT 26-JAN-2000 (first entry)
DE Anti-tissue factor mouse monoclonal antibody ATR-2 H chain V region.
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric.
OS Synthetic.
OS Mus sp.
XX
PN WO9951743-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-JP001768.
XX
PR 03-APR-1998; 98JP-00091850.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
PI Sato K, Adachi H, Yabuta N;
DR WPI; 1999-620204/53.
DR N-PSDB; AAZ33006.
XX
PT Humanised antibody recognizing human tissue factor, used for treatment of
PT disseminated intravascular coagulation.
PS Claim 1; Page 274; 291pp; Japanese.
XX
CC The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment

```
CC   and prevention of thrombotic disease, especially of disseminated
CC   intravascular coagulation (DIC). The humanised antibody has the high hTF
CC   binding activity of the mouse monoclonal antibody but greatly reduced
CC   immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 118 AA;

Query Match             86.5%;  Score 560.5; DB 2; Length 118;
Best Local Similarity   89.9%;  Pred. No. 5.7e-40;
Matches 107; Conservative    4; Mismatches    7; Indels    1; Gaps    1;

Qy          1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||||||||||||| | |||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60

Qy         61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
              :|||||||||||||||||| :|||||||||||||||||||||:|| ||||||||||||||
Db         61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLTVSS 118
```

```
RESULT 2
AAY52756
ID   AAY52756 standard; protein; 118 AA.
XX
AC   AAY52756;
XX
DT   26-JAN-2000  (first entry)
XX
DE   Anti-tissue factor mouse monoclonal antibody ATR-3 H chain V region.
XX
KW   Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW   ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW   disseminated intravascular coagulation; immunogenicity; chimeric.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO9951743-A1.
XX
PD   14-OCT-1999.
XX
PF   02-APR-1999;  99WO-JP001768.
XX
PR   03-APR-1998;  98JP-00091850.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Sato K, Adachi H, Yabuta N;
XX
DR   WPI; 1999-622004/53.
DR   N-PSDB; AAZ33007.
XX
PT   Humanised antibody recognizing human tissue factor, used for treatment of
PT   disseminated intravascular coagulation.
XX
PS   Claim 1; Page 275; 291pp; Japanese.
XX
CC   The present invention describes chimeric antibody (Ab) heavy (H) chains
CC   containing the variable region of the H chain of a mouse monoclonal Ab
CC   recognising human tissue factor (hTF) and the constant region of the H
CC   chain of a human Ab. The variable region is one of six specified
CC   sequences (which are the H chain variable regions from mouse monoclonal
CC   Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
CC   containing the variable region of the L chain of a mouse monoclonal
CC   Ab recognising human tissue factor (hTF) and the constant region of the L
CC   chain of a human Ab, the variable region being one of six specified
CC   sequences (which are the L chain variable regions from mouse monoclonal
CC   Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC   and prevention of thrombotic disease, especially of disseminated
CC   intravascular coagulation (DIC). The humanised antibody has the high hTF
CC   binding activity of the mouse monoclonal antibody but greatly reduced
CC   immunogenicity. AAZ33091 and Y527007 to AAY52767 represent
```

```
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 118 AA;

Query Match             86.5%;  Score 560.5; DB 2; Length 118;
Best Local Similarity   89.9%;  Pred. No. 5.7e-40;
Matches 107; Conservative    4; Mismatches    7; Indels    1; Gaps    1;

Qy          1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
              ||||||||||||||||||||||||||||||| | |||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60

Qy         61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
              :|||||||||||||||||| :|||||||||||||||||||||:|| ||||||||||||||
Db         61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGE-GYYFDYWGQGTTLTVSS 118
```

```
RESULT 3
ABR82930
ID   ABR82930 standard; protein; 120 AA.
XX
AC   ABR82930;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Anti-human tenascin ST2146 MAb heavy chain variable region (VH).
XX
KW   ST2146; tenascin C; monoclonal antibody; EGF; epidermal growth factor;
KW   cytostatic; antibody therapy; vaccine.
XX
OS   Synthetic.
XX
PN   WO200307260B-A1.
XX
PD   04-SEP-2003.
XX
PF   20-FEB-2003;  2003WO-IT000098.
XX
PR   26-FEB-2002;  2002US-0359299P.
XX
PA   (SIGT ) SIGMA-TAU IND FARM RIUNITE SPA.
XX
PI   De Santis R, Anastasi AM;
XX
DR   WPI; 2003-679945/64.
DR   N-PSDB; ACF36519, ACF36531.
XX
PT   New anti-human tenascin ST2146 monoclonal antibody, and its proteolytic
PT   fragments that bind to an antigenic epitope within the EGF-like repeat of
PT   human tenascin C, useful for treating tumors, e. g. gliomas, cystic brain
PT   tumors.
XX
PS   Claim 1; Fig 11; 55pp; English.
XX
CC   The invention relates to an anti-human tenascin ST2146 monoclonal
CC   antibody (MAb) whose light and heavy chain variable region sequences and
CC   their proteolytic fragments that bind to an antigenic epitope within the
CC   EGF (epidermal growth factor)-like repeat of human tenascin C. The
CC   antibody, its fragment, recombinant or conjugate derivatives,
CC   immunoglobulin molecule and biotinylated derivatives are useful for a
CC   diagnostic means for detecting, or preparing a medicament for treating,
CC   diseases expressing tenascin, e.g. tumor such as gliomas, mammary, cystic
CC   brain tumours, lung carcinomas, fibrosarcomas, and squamous cell
CC   carcinomas. The diagnostic means is used in the form of a kit suitable for
CC   three-step pre-targeting method. The antibody, in combination with a
CC   second tenascin-specific antibody are useful in sandwich assay for
CC   detecting the level of circulating tenascin. The present sequence
CC   represents the ST2146 MAb heavy chain variable region sequence
XX
SQ   Sequence 120 AA;

Query Match             84.6%;  Score 548.5; DB 7; Length 120;
```

Best Local Similarity 86.7%; Pred. No. 6e-39; 6; Mismatches 9; Indels 1; Gaps 1;
Matches 104; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        :::||||||||||||||||||.|||:|||:|||:|||||||||||||||||||||||||
Db   1 KVKLQQSGPELVKPGASVKVSCKASGYAFTSYNMYWVKQSHGKSLEWIGYIDPYNGVTSY 60

Qy   61 SQKFRGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGNFPYY-FDYWGQGTTLTVSS 119
        :||||||||||||||||||||||||||||||||||||||||||| ||||||:|||||
Db   61 NQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGGSIYAMDYWGQGTTVTVSS 120

Qy   Synthetic.
Db   Mus sp.

RESULT 4
ID   ADC24943 standard; protein; 140 AA.
XX
AC   ADC24943;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Mouse 19/2 antibody heavy chain variable region SEQ ID NO:28.
XX
KW   fusion protein; chimerised antibody; tumour necrosis factor; TNF;
KW   antibody; chimeric fusion protein; antiinflammatory; antirheumatic;
KW   antiarthritic; antipsoriatic; antiasthmatic; neuroprotective; virucide;
KW   antibacterial; immunosuppressive; nephrotropic; antiarteriosclerotic;
KW   rheumatoid arthritis; inflammatory condition; psoriasis; asthma;
KW   inflammatory bowel disease; multiple sclerosis; viral pneumonia;
KW   bacterial pneumonia; septic shock; nephritis; arteriosclerosis; mouse;
KW   19/2 antibody.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO2003068924-A2.
XX
PD   21-AUG-2003.
XX
PF   12-FEB-2003; 2003WO-US004243.
XX
PR   13-FEB-2002; 2002US-035S838P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Renner C, Scott A;
XX
DR   WPI; 2003-679629/64.
DR   N-PSDB; ADC24998.
XX
PT   New nucleic acid, useful for producing humanized or chimeric antibodies,
PT   or fusion proteins comprising the antibodies, which are G250-specific and
PT   useful for treating inflammatory conditions, e.g. rheumatoid arthritis or
PT   asthma.
XX
PS   Example 2; SEQ ID NO 28; 80pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule, which
CC   encodes a fusion protein comprising a chimerised antibody molecule, and a
CC   tumour necrosis factor (TNF) molecule or its fragment. The antibody
CC   specifically binds to a target. The fragment of the TNF molecule
CC   possesses the cell killing properties of a full-length TNF molecule. Also
CC   described: (1) a chimeric fusion protein (I) encoded by the isolated
CC   nucleic acid molecule; (2) an expression vector comprising the isolated
CC   nucleic acid molecule operably linked to a promoter; and (3) a
CC   recombinant cell comprising the isolated nucleic acid molecule or the
CC   expression vector. (I) has antiinflammatory, antirheumatic,
CC   antiarthritic, antipsoriatic, antiasthmatic, neuroprotective,
CC   antibacterial, immunosuppressive, nephrotropic and antiarteriosclerotic
CC   activities. The nucleic acid is useful for the expression of proteins,
CC   especially antibodies, as well as fusion proteins that incorporate the
CC   antibodies and a protein. The expression vector is useful in manufacturing
CC   a recombinant antibody (e.g. a fully human, humanized or chimeric
CC   antibody) in a eukaryotic cell. The antibody is useful in therapy,

CC   particularly for targeting G250 and blocking granulocyte-macrophage
CC   stimulating factor (GM-CSF), which is involved in the development of
CC   rheumatoid arthritis. The antibody is useful for treating inflammatory
CC   conditions, e.g. psoriasis, asthma, inflammatory bowel disease, multiple
CC   sclerosis, viral or bacterial pneumonia, septic shock, nephritis, or
CC   arteriosclerosis. The present sequence represents mouse 19/2 antibody
CC   heavy chain variable region, which is used in an example from the present
CC   invention.
XX
SQ   Sequence 140 AA;

Query Match   83.5%; Score 541; DB 7; Length 140;
Best Local Similarity 82.4%; Pred. No. 3.1e-38;
Matches 98; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        :.|||||||||||||||||||||:|||:||||:|:||||||||||||||||||||||||
Db   18 EVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSHGKSLDWIGYIAPYSGGTGY 77

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
        :.||||||||||||||||||||:|:|||||||||||||||| |||| ||
Db   78 NQBFKDRATLTVDKSSSTAYMELRSLTSDDSAVYYCARRDRPFYYFDYWGQGTTLRVSS 136

Qy   Murine 19/2 heavy chain variable region protein.
Db   Mus sp.

RESULT 5
ID   ADK51711 standard; protein; 140 AA.
XX
AC   ADK51711;
XX
DT   06-MAY-2004 (first entry)
XX
DE   Murine 19/2 heavy chain variable region protein.
XX
KW   granulocyte macrophage colony stimulating factor; GM-CSF; antibody;
KW   antiinflammatory; antiarthritic; antirheumatic; rheumatoid arthritis;
KW   inflammatory disease; murine; 19/2 heavy chain variable region; mouse.
XX
OS   Mus sp.
XX
PN   WO2003068920-A2.
XX
PD   21-AUG-2003.
XX
PF   12-FEB-2003; 2003WO-US004185.
XX
PR   13-FEB-2002; 2002US-035S838P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Renner C, Scott A, Burgess A;
XX
DR   WPI; 2003-679625/64.
DR   N-PSDB; ADK51710.
XX
PT   Nucleic acids encoding chimeric granulocyte macrophage colony stimulating
PT   factor (GM-CSF) specific antibodies comprising a light and a heavy chain,
PT   useful for blocking effects of GM-CSF on cells, e.g. in preventing
PT   rheumatoid arthritis.
XX
PS   Example 2; SEQ ID NO 28; 81pp; English.
XX
CC   The invention relates to an isolated nucleic acid encoding a chimerised
CC   granulocyte macrophage colony stimulating factor (GM-CSF) specific
CC   antibody light chain or heavy chain. The invention further relates to: a
CC   chimerised granulocyte macrophage colony stimulating factor (GM-CSF)
CC   specific antibody light chain encoded by nucleotides 1357-1752 of a
CC   defined sequence of 6159 bp concatenated to the amino acid sequence
CC   encoded by nucleotides 1886-2203 of the 6159bp sequence; or a chimerised
CC   GM-CSF specific antibody heavy chain encoded by nucleotides 1357-1764 of
CC   a defined 6629 bp sequence concatenated to the amino acid sequence
CC   encoded by nucleotides 1839-2825 of the 6629bp sequence. The GM-CSF
CC   antibodies have antiinflammatory, antiarthritic, and antirheumatic

```
CC    activities. The GM-CSF nucleic acid is useful for blocking GM-CSF and its
CC    effects on cells, such as in preventing the development of rheumatoid
CC    arthritis and other inflammatory diseases and conditions. This sequence
CC    represents the murine 19/2 heavy chain variable region protein of the
CC    invention.
XX
SQ    Sequence 140 AA;

Query Match             83.5%;  Score 541; DB 7;  Length 140;
Best Local Similarity   82.4%;  Pred. No. 3.1e-38;
Matches  98;  Conservative  10;  Mismatches  11;  Indels   0;  Gaps   0;

Qy      1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
           ||||||||||||||||||||||||||||||||| || ||||||||||||||| ||| |
Db     18  EVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSHGKSLDWIGYIAPYSGGTGY 77

Qy     61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
           :|||||||||||||||||||||||  :|:|||||||||| |||||||||||||| |||
Db     78  NQEFKNRATLTVDKSSSTAYMELRSLTSDDSAVYYCARRDRFPYYFDYWGQGTTLRVSS 136
```

RESULT 6
AAW95481

```
ID   AAW95481 standard; protein; 116 AA.
XX
AC   AAW95481;
XX
DT   29-MAR-1999  (first entry)
XX
DE   Mouse derived RT3 phage antibody heavy chain pattern A genetic sequence.
XX
KW   Catalytic; antibody; phage display; immunising; phage expression vector;
KW   prodrug; scFv.
XX
OS   Mus sp.
XX
XX
PN   US5855885-A.
XX
PD   05-JAN-1999.
XX
PF   14-JUL-1994;  94US-00273146.
XX
PR   22-JAN-1993;  93US-00007684.
XX
PA   (MCCA/)  MCCAFFERTY J.
PA   (CHIS/)  CHISWELL D.
PA   (DARS/)  DARSLEY M J.
PA   (TITM/)  TITMAS R C.
PA   (MART/)  MARTIN M T.
PA   (KENT/)  KENTEN J H.
PA   (SMIT/)  SMITH R.
PA   (FITZ/)  FITZGERALD K.
PA   (WILL/)  WILLIAMS R O.
XX
PI   Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
PI   Kenten JH, Chiswell D, Mccafferty J, Titmas RC;
XX
DR   WPI; 1999-105036/09.
DR   N-PSDB; AAX00880.
XX
PT   Production of catalytic antibodies displayed on bacteriophages -
PT   comprises generating a gene library of antibody-derived domains inserting
PT   coding into a phage expression vector and isolating the catalytic
PT   antibodies.
XX
PT   The invention relates to methods for producing catalytic antibodies
PT   displayed on a phage. The method comprises: (a) generating a gene library
PT   of antibody-derived domains; (b) inserting coding for the domains into a
PT   phage expression vector; and (c) isolating the catalytic antibodies. The
PT   phage expression vector incorporates a histidine peptide in tandem with a
PT   myc peptide. The catalytic antibodies can be isolated by preparing an
PS   Example 4; Fig 12A-J; 117pp; English.
```

```
CC    antigen; optionally immunising an animal with the antigen; generating a
CC    library of VH and VL domains from the immunised animal; cloning the VH
CC    and VL domains into a phage expression vector to generate phage display
CC    antibodies; selecting phage display antibodies which bind specifically to
CC    the antigen; screening the selected phage display antibodies for
CC    catalytic activity to substrate; and isolating the catalytic antibodies,
CC    where the phage expression vector incorporates a histidine peptide in
CC    tandem with a myc peptide. The processes are used to produce catalytic
CC    antibodies, which can be used for in vivo activation of a prodrug. The
CC    present sequence represents a genetic sequence of heavy chain pattern A
CC    from mouse derived RT3 phage antibodies
XX
SQ    Sequence 116 AA;

Query Match             81.7%;  Score 529.5; DB 2;  Length 116;
Best Local Similarity   85.7%;  Pred. No. 2.4e-37;
Matches 102;  Conservative   6;  Mismatches   8;  Indels   3;  Gaps   2;

Qy      1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
           :|||||||||||||||||||||||||||||||| |||||||||||||||||||| |
Db      1  QVQLQQSGPELVKPGASVKVSCKASGYAFTNYNIYWVKQSHGKSLEWIGYIDPYSGGSSY 60

Qy     61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
           :|||||||||||||||||||||||||||||||||||| |  ||: | |||||| ||||
Db     61  NQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCA--GGNP-RFAFWGQGTTVTVSS 116
```

RESULT 7
AAW84093

```
ID   AAW84093 standard; protein; 117 AA.
XX
AC   AAW84093;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Murine vitronectin alpha-v beta-3 receptor MAb VH region.
XX
KW   Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW   mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
KW   metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;
KW   diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
KW   Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
KW   immunotherapy.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          31..35
FT                   /label= CDR1
FT   Region          50..66
FT                   /label= CDR2
FT   Region          99..106
FT                   /label= CDR3
XX
PN   WO9840488-A1.
XX
PD   17-SEP-1998.
XX
PF   12-MAR-1998;  98WO-US004987.
XX
PR   12-MAR-1997;  97US-0039609P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Jonak ZL, Johanson KO, Taylor AH;
XX
DR   WPI; 1999-034590/03.
XX
PT   New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT   immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory
PT   disorders, atherosclerosis, restenosis, cancers or osteoporosis.
XX
PS   Example 13; Page 56; 97pp; English.
```

XX
CC This is the amino acid sequence of the heavy chain variable region (VH)
CC of the anti-human alpha-v beta-3 vitronectin receptor murine monoclonal
CC antibody D12, as deduced from isolated cDNA (see AAV1797). D12 VH and VL
CC (see AAW84094) show sequence similarity to Kabat VH subgroup III (see
CC AAW84095) and Kabat VK subgroup III (see AAW84096), respectively.
CC Humanised VH (see AAW84097) and VL (see AAW84098) were constructed by
CC combining the framework regions of the human V region consensus sequences
CC with complementarity determining regions of D12 (keeping some preferred
CC murine framework residues). The humanised antibodies are specifically
CC reactive with the human alpha-v beta-3 protein receptor and capable of
CC neutralising the receptor. They can be used for passive immunotherapy of
CC a disorder mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
CC disorders or angiogenic-related disorders, such as angiogenesis
CC associated with diabetic retinopathy, atherosclerosis and restenosis,
CC chronic inflammatory disorders, macular degeneration, rheumatoid
CC arthritis and cancer, e.g. solid tumour metastasis, and diseases where
CC bone resorption is associated with pathology such as osteoporosis,
CC hyperparathyroidism, Paget's disease, hypercalcemia of malignancy,
CC osteolytic lesions produced by bone metastasis, bone loss due to
CC immobilisation or sex hormone deficiency. They can also be used for
CC targeted drug therapy, and for detection and diagnosis
XX
SQ Sequence 117 AA;

Query Match   81.6%; Score 529; DB 2; Length 117;
Best Local Similarity   84.3%;
Matches 102; Conservative   8; Mismatches   5; Indels   6; Gaps   2;

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARR--GNPYYFDYWGQGTTLTVS 118
        |||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db 61 NQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVFYCARQNYGSFA----YWGQGTLVTVS 116

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMMVWVKQSHGKSLEWIGYIDPYYGDPGY 60
        ||||||||||:|:||||||||||||||:|:::|||||||||||||||||||||||:|:|
Db   1 EIQLQQSGPEVVKPGASVKVSCKASGYAFTSYNMTWVKQSHGKSLEWIGYIDPYNGDTFY 60

Qy 119 S 119
          :
Db 117 A 117

RESULT 8
ID ABP96759 standard; protein; 214 AA.
AC ABP96759;
DT 05-JUN-2003 (first entry)
DE TSH receptor antibody 17D2 heavy chain amino acid sequence.
OS Synthetic.
KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.
PN WO2003018632-A2.
PD 06-MAR-2003.
PA (RSRR-) RSR LTD.
PI Smith BR, Furmaniak J, Sanders JF;
PR 01-JUL-2002; 2002GB-0015212.
PR 23-AUG-2001; 2001GB-0020649.
PF 21-AUG-2002; 2002WO-GB003831.
DR WPI; 2003-290051/28.
DR N-PSDB; ACC44914.

XX
PT New polypeptide sequence having part or all of the primary structural
PT conformation of one or more TSH receptor epitopes, useful for treating an
PT autoimmune disease associated with an immune reaction to a TSH receptor,
PT e.g. thyroid cancer.
XX
PS Claim 71; Fig 17; 196pp; English.
XX
CC The present invention describes a polypeptide sequence comprising part or
CC all of the primary structural conformation of one or more thyrotropin
CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC produced in response to a TSH receptor interact. Also described: (1) one
CC or more receptor TSH epitopes with which the autoantibodies and/or
CC lymphocytes interact, as with the polypeptide sequence described above;
CC (2) a method of screening for autoantibodies or lymphocytes produced in
CC response to a TSH receptor in a sample of body fluid obtained from a
CC subject suspected of suffering from, susceptible to, having or recovering
CC from autoimmune disease associated with an immune reaction to a TSH
CC receptor; (3) a binding partner for a TSH receptor, which is capable of
CC binding to a TSH receptor to stimulate the TSH receptor, where the
CC binding partner does not comprise TSH or naturally produced antibodies to
CC the TSH receptor; and (4) a combination comprising the binding partner
CC and one or more further agents capable of stimulating thyroid tissue,
CC and/or tissue containing a TSH receptor, for simultaneous, separate or
CC sequential use in stimulating thyroid tissue, and/or tissue containing a
CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC gene therapy. The polypeptide, compositions and methods from the present
CC invention can be used for treating an autoimmune disease associated with
CC an immune reaction to a TSH receptor. The specific binding partner is
CC useful for the manufacture of a medicament for stimulating thyroid tissue
CC or tissue containing a TSH receptor, and for treating thyroid cancer.
CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC and VL domains given in ABP96751 to ABP96778, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 214 AA;

Query Match   81.1%; Score 525.5; DB 6; Length 214;
Best Local Similarity   81.7%;
Matches   98; Conservative 11; Mismatches 10; Indels   1; Gaps   1;

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNF-PYYFDYWGQGTTLTVSS 119
        |||||||||||||||||||||| |||||||||||||||: || || ||||||||||||
Db 61 HQKFKGKATLTVDKSSSTAYMRLNSLTSEDSAVYYCARRWDWDPYAMDYWGQGTSVTVSS 120

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMMVWVKQSHGKSLEWIGYIDPYYGDPGY 60
        ||:||||||||||:||||||||||||||:||||||||||||||||||||||:||||:||
Db   1 DVQIQQSGPELVKPGASVKMSCKASGYSFTAYNMHWVKQTHGKSLEWIGYIDPYSGATSY 60

RESULT 9
ID ABP96760 standard; protein; 214 AA.
AC ABP96760;
DT 05-JUN-2003 (first entry)
DE TSH receptor antibody 17D2 heavy chain amino acid sequence.
OS Synthetic.
KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.
PN WO2003018632-A2.
PD 06-MAR-2003.
PF 21-AUG-2002; 2002WO-GB003831.
XX

PR   23-AUG-2001; 2001GB-00020649.
PR   01-JUL-2002; 2002GB-0015212.
XX
PA   (RSRR-) RSR LTD.
XX
PI   Smith BR, Furmaniak J, Sanders JF;
XX
DR   WPI; 2003-290051/28.
DR   N-PSDB; ACC44915.
XX
PT   New polypeptide sequence having part or all of the primary structural
PT   conformation of one or more TSH receptor epitopes, useful for treating an
PT   autoimmune disease associated with an immune reaction to a TSH receptor,
PT   e.g. thyroid cancer.
XX
PS   Claim 67; Fig 18; 196pp; English.
XX
CC   The present invention describes a polypeptide sequence comprising part or
CC   all of the primary structural conformation of one or more thyrotropin
CC   (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC   produced in response to a TSH receptor interact. Also described: (1) one
CC   or more receptor TSH epitopes with which the autoantibodies and/or
CC   lymphocytes interact, as with the polypeptide sequence described above;
CC   (2) a method of screening for autoantibodies or lymphocytes produced in
CC   response to a TSH receptor in a sample of body fluid obtained from a
CC   subject suspected of suffering from, susceptible to, having or recovering
CC   from autoimmune disease associated with an immune reaction to a TSH
CC   receptor; (3) a binding partner for a TSH receptor, which is capable of
CC   binding to a TSH receptor to stimulate the TSH receptor, where the
CC   binding partner does not comprise TSH or naturally produced antibodies to
CC   the TSH receptor; and (4) a combination comprising the binding partner
CC   and one or more further agents capable of stimulating thyroid tissue
CC   and/or tissue containing a TSH receptor, for simultaneous, separate or
CC   sequential use in stimulating thyroid tissue, and/or tissue containing a
CC   TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC   gene therapy. The polypeptide, compositions and methods from the present
CC   invention can be used for treating an autoimmune disease associated with
CC   an immune reaction to a TSH receptor. The specific binding partner is
CC   useful for the manufacture of a medicament for stimulating thyroid tissue
CC   or tissue containing a TSH receptor. The specific binding partner is
CC   ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC   sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC   and VL domains given in ABP96751 to ABP96778, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 214 AA;

Query Match   81.1%; Score 525.5; DB 6; Length 214;
Best Local Similarity   81.7%; Pred. No. 9.7e-37;
Matches   98; Conservative   11; Mismatches   10; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGPDGY 60
              ::|:||||||||||||||||||||||||:||||||||:||||||||||||:||||||
Db   1 DVQIQQSGPELVKPGASVKMSCKASGYSFTAYNMHWVKQTHGKSLEWIGYIDPYSGATSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNF-PYYFDYWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||:: ||||||||||||||||||
Db   61 HQKFKGKATLTVDKSSSTAYMRLNSLTSEDSAVYYCARRWDWDPYAMDYWGQGTSVTVSS 120

RESULT 10
ABP96763
ID   ABP96763 standard; protein; 214 AA.
XX
AC   ABP96763;
XX
DT   05-JUN-2003 (first entry)
XX
DE   TSH receptor antibody 14D3 heavy chain amino acid sequence.
XX
KW   Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW   autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW   gene therapy; immune reaction; thyroid cancer.
XX

XX
OS   Synthetic.
XX
PN   WO200301863Z-A2.
XX
PD   06-MAR-2003.
XX
PF   21-AUG-2002; 2002WO-GB003831.
XX
PR   23-AUG-2001; 2001GB-00020649.
PR   01-JUL-2002; 2002GB-0015212.
XX
PA   (RSRR-) RSR LTD.
XX
PI   Smith BR, Furmaniak J, Sanders JF;
XX
DR   WPI; 2003-290051/28.
DR   N-PSDB; ACC44918.
XX
PT   New polypeptide sequence having part or all of the primary structural
PT   conformation of one or more TSH receptor epitopes, useful for treating an
PT   autoimmune disease associated with an immune reaction to a TSH receptor,
PT   e.g. thyroid cancer.
XX
PS   Claim 71; Fig 21; 196pp; English.
XX
CC   The present invention describes a polypeptide sequence comprising part or
CC   all of the primary structural conformation of one or more thyrotropin
CC   (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC   produced in response to a TSH receptor interact. Also described: (1) one
CC   or more receptor TSH epitopes with which the autoantibodies and/or
CC   lymphocytes interact, as with the polypeptide sequence described above;
CC   (2) a method of screening for autoantibodies or lymphocytes produced in
CC   response to a TSH receptor in a sample of body fluid obtained from a
CC   subject suspected of suffering from, susceptible to, having or recovering
CC   from autoimmune disease associated with an immune reaction to a TSH
CC   receptor; (3) a binding partner for a TSH receptor, which is capable of
CC   binding to a TSH receptor to stimulate the TSH receptor, where the
CC   binding partner does not comprise TSH or naturally produced antibodies to
CC   the TSH receptor; and (4) a combination comprising the binding partner
CC   and one or more further agents capable of stimulating thyroid tissue
CC   and/or tissue containing a TSH receptor, for simultaneous, separate or
CC   sequential use in stimulating thyroid tissue, and/or tissue containing a
CC   TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC   gene therapy. The polypeptide, compositions and methods from the present
CC   invention can be used for treating an autoimmune disease associated with
CC   an immune reaction to a TSH receptor. The specific binding partner is
CC   useful for the manufacture of a medicament for stimulating thyroid tissue
CC   or tissue containing a TSH receptor, and for treating thyroid cancer.
CC   ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC   sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC   and VL domains given in ABP96751 to ABP96778, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 214 AA;

Query Match   80.3%; Score 520.5; DB 6; Length 214;
Best Local Similarity   80.0%; Pred. No. 2.6e-36;
Matches   96; Conservative   13; Mismatches   10; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGPDGY 60
              ::|:|:|| ||||||||||:|:||||||||:||||||||||||||||||||||||||
Db   1 DVQMQQPGPELVKPGASLKMSCKASGYSFTGYAMHWVKQSHGKSLEWIGYIDPYSGATSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNF-PYYFDYWGQGTTLTVSS 119
              |||||||||||||||||||||:||||||||||||||||:: ||||||||||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARRWDWDPYANDYWGQGTSVTVSS 120

RESULT 11
ABP96764
ID   ABP96764 standard; protein; 214 AA.
XX

AC   ABP9764;
XX
DT   05-JUN-2003 (first entry)
XX
DE   TSH receptor antibody 14D3 heavy chain amino acid sequence.
XX
KW   Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW   autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW   gene therapy; immune reaction; thyroid cancer.
XX
OS   Synthetic.
XX
PN   WO200301B632-A2.
XX
PD   06-MAR-2003.
XX
PF   21-AUG-2002; 2002WO-GB003831.
XX
PR   23-AUG-2001; 2001GB-00020649.
PR   01-JUL-2002; 2002GB-0015212.
XX
PA   (RSRR-) RSR LTD.
XX
PI   Smith BR, Furmaniak J, Sanders JF;
XX
DR   WPI; 2003-290051/28.
DR   N-PSDB; ACC44919.
XX
PT   New polypeptide sequence having part or all of the primary structural
PT   conformation of one or more TSH receptor epitopes, useful for treating an
PT   autoimmune disease associated with an immune reaction to a TSH receptor,
PT   e.g. thyroid cancer.
XX
PS   Claim 67; Fig 22; 196pp; English.
XX
CC   The present invention describes a polypeptide sequence comprising part or
CC   all of the primary structural conformation of one or more thyrotropin
CC   (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC   produced in response to a TSH receptor interact. Also described: (1) one
CC   or more receptor TSH epitopes with which the autoantibodies and/or
CC   lymphocytes interact, as with the polypeptide sequence described above;
CC   (2) a method of screening for autoantibodies or lymphocytes produced in
CC   response to a TSH receptor in a sample of body fluid obtained from a
CC   subject suspected of suffering from, susceptible to, having or recovering
CC   from autoimmune disease associated with an immune reaction to a TSH
CC   receptor; (3) a binding partner for a TSH receptor, which is capable of
CC   binding to a TSH receptor to stimulate the TSH receptor, where the
CC   binding partner does not comprise TSH or naturally produced antibodies to
CC   the TSH receptor; and (4) a combination comprising the binding partner
CC   and one or more further agents capable of stimulating thyroid tissue,
CC   and/or tissue containing a TSH receptor, for simultaneous, separate or
CC   sequential use in stimulating thyroid tissue, and/or tissue containing a
CC   TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC   gene therapy. The polypeptide, compositions and methods from the present
CC   invention can be used for treating an autoimmune disease associated with
CC   an immune reaction to a TSH receptor. The specific binding partner is
CC   useful for the manufacture of a medicament for stimulating thyroid tissue
CC   or tissue containing a TSH receptor, and for treating thyroid cancer.
CC   ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC   sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC   and VL domains given in ABP96751 to ABP96778, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 214 AA;

Qy   1 EIQLCQOSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
               :||||||||||||||||||||||||||:|::||||||||||||||||||||||||||||||
Db   1 DVQMQQPGPELVKPGASLRMSCKASGYSFTCYNMHWVKQSHGKSLEWIGYIDPYYSGATSY 60

Query Match   80.3%; Score 520.5; DB 6; Length 214;
Best Local Similarity   80.0%; Pred. No. 2.6e-36;
Matches   96; Conservative 13; Mismatches 10; Indels   1; Gaps   1;

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNP-PYYFDYWGQGTTLTVSS 119
               || ||||||||||||||||||||| :|||| |||||||||||| | |||||||||||||||
Db   61 NQKFBGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARRWDPYAMDYWGQGTSVTVSS 120

RESULT 12
ADC79231
ID   ADC79231 standard; protein; 239 AA.
XX
AC   ADC79231;
XX
DT   01-JAN-2004 (first entry)
XX
DE   Anti-CA125 scFvs VK-8-1.9 amino acid sequence.
XX
KW   CA 125 tumour antigen; CA 125 tumour antigen modulator;
KW   CA 125 tumour antigen-associated disease; cytostatic; gene therapy.
XX
OS   Synthetic.
XX
PN   WO2003076465-A2.
XX
PD   18-SEP-2003.
XX
PF   11-MAR-2003; 2003WO-CA000341.
XX
PR   11-MAR-2002; 2002US-0363306P.
PR   28-FEB-2003; 2003CA-02420494.
XX
PI   Rancourt C, Piche A, Beaudin J;
XX
DR   WPI; 2003-722323/68.
XX
PS   Disclosure; Fig 29C; 90pp; English.
XX
PT   New modulator capable of negatively modulating a CA 125 tumor antigen in
PT   a mammalian cell, useful for preparing a composition for preventing or
PT   treating CA 125 tumor antigen-associated disease in a mammal.
XX
CC   The present invention describes a modulator capable of negatively
CC   modulating a CA 125 tumour antigen in a mammalian cell. Also described:
CC   (1) a recombinant nucleic acid comprising at least one sequence selected
CC   from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
CC   ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
CC   acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
CC   or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
CC   negatively modulating a CA 125 tumour antigen in a mammalian cell. A
CC   modulator capable of negatively modulating a CA 125 tumour antigen has
CC   cytostatic activity, and can be used in gene therapy. The modulator,
CC   recombinant nucleic acid, vector or host cell can be used for preparing a
CC   composition for preventing or treating CA 125 tumour antigen-associated
CC   disease in a mammal. The present sequence is used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 239 AA;

Qy   1 EIQLCQOSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
               :||||||||||||||||||:|||||||:||||||||||||||||||||||||||||||||||
Db   1 QVQLQESGPELVKPGASVKISCKASGYTFTDYNMHWVKQSHGKSLEWIGYIYPYNGDTGY 60

Query Match   80.0%; Score 518.5; DB 7; Length 239;
Best Local Similarity   80.7%; Pred. No. 4.2e-36;
Matches   96; Conservative 11; Mismatches 11; Indels   1; Gaps   1;

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPPYYFDYWGQGTTLTVSS 119
               || |||||||||||||||| ||||||||||||||||||||||| | |||||||||||||||
Db   61 NQKFRNKASLTVDTSSSTAYMELRSLTSEDSAVYYCARSGGP-WYFDVWGQGTTVVSS 118

RESULT 13
ADC27445

RESULT 14
ID   ABP96756 standard; protein; 214 AA.
XX
AC   ABP96756;
XX

ID   ADC27445 standard; protein; 117 AA.
XX
AC   ADC27445;
XX
DT   18-DEC-2003 (first entry)
XX
DE   TMEFF2#20 heavy chain variable region SEQ ID NO:14.
XX
KW   TMEFF2#19; TMEFF2; binding inhibitor; prostate cancer;
KW   antibody; vaccine; primary prostate cancer; metastatic prostate cancer;
KW   cytostatic; locally advanced prostate cancer; androgen independent prostate cancer.
XX
OS   Synthetic.
XX
PN   WO200307585S-A2.
XX
PD   18-SEP-2003.
XX
PF   07-MAR-2003; 2003WO-US007209.
XX
PR   08-MAR-2002; 2002US-0362837P.
PR   27-DEC-2002; 2002US-0436812P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Bhaskar V, De La Calle A, Law D, Caras I, Ramakrishnan V;
PI   Murray R, Afar D, Powers D;
XX
DR   WPI; 2003-756783/71.
DR   N-PSDB; ADC27444.
XX
PT   New antibody that competitively inhibits binding prostate cancer, e.g. primary, metastatic, locally
PT   advanced, or androgen independent prostate cancer.
XX
PS   Example 1; SEQ ID NO 14; 51pp; English.
XX
CC   The present invention describes an antibody (I) that competitively
CC   inhibits binding of TMEFF2#19 to TMEFF2. Also described: (1) a
CC   pharmaceutical composition comprising the antibody and a carrier; (2)
CC   detecting a prostate cancer cell in a biological sample from a patient by
CC   contacting the biological sample with the antibody; (3) inhibiting
CC   proliferation of a prostate cancer-associated cell by contacting the cell
CC   with the antibody; and (4) treating prostate cancer with an antibody to
CC   TMEFF2. (I) has cytostatic activity and can be used in vaccines. The
CC   antibody, composition and method are useful for treating prostate cancer,
CC   e.g. primary prostate cancer, metastatic prostate cancer, locally
CC   advanced prostate cancer, androgen independent prostate cancer, prostate
CC   cancer that has been treated with neoadjuvant therapy, or prostate cancer
CC   that is refractory to treatment with neoadjuvant therapy. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 117 AA;

Query Match   79.8%; Score 517; DB 7; Length 117;
Best Local Similarity   82.4%; Pred. No. 2.8e-36;
Matches   98; Conservative   9; Mismatches   10; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        |||||||||||:|||||||:||||| :||:||:||||||||:|||||||||||::|| ||
Db   1 EIQLQQSGPELMKPGASVKISCKASTYSFTRYFMHWVKQSHGESLEWIGYIDPFNGGTGY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAARGNFPYYFDYWGQGTTLTVSS 119
        ||||||||||||||||||||||:|||||||||||||||| |: ||||||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYYCVTYGS--DYFDYWGQGTTLTVSS 117

DT   05-JUN-2003 (first entry)
XX
DE   TSH receptor antibody 16B5 heavy chain amino acid sequence.
XX
KW   Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW   autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW   gene therapy; immune reaction; thyroid cancer.
XX
OS   Synthetic.
XX
PN   WO200301863Z-A2.
XX
PD   06-MAR-2003.
XX
PF   21-AUG-2002; 2002WO-GB003831.
XX
PR   23-AUG-2001; 2001GB-00020649.
PR   01-JUL-2002; 2002GB-00015212.
XX
PA   (RSRR-) RSR LTD.
XX
PI   Smith BR, Furmaniak J, Sanders JF;
XX
DR   WPI; 2003-290051/28.
DR   N-PSDB; ACC44911.
XX
PT   New polypeptide sequence having part or all of the primary structural
PT   conformation of one or more TSH receptor epitopes, useful for treating an
PT   autoimmune disease associated with an immune reaction to a TSH receptor,
PT   e.g. thyroid cancer.
XX
PS   Claim 67; Fig 14; 196pp; English.
XX
CC   The present invention describes a polypeptide sequence comprising part or
CC   all of the primary structural conformation of one or more thyrotropin
CC   (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC   produced in response to a TSH receptor interact. Also described: (1) one
CC   or more receptor TSH epitopes with which the autoantibodies and/or
CC   lymphocytes interact, as with the polypeptide sequence described above;
CC   (2) a method of screening for autoantibodies or lymphocytes produced in
CC   response to a TSH receptor in a sample of body fluid obtained from a
CC   subject suspected of suffering from, susceptible to, having or recovering
CC   from autoimmune disease associated with an immune reaction to a TSH
CC   receptor; (3) a binding partner for a TSH receptor, which is capable of
CC   binding to a TSH receptor to stimulate the TSH receptor, where the
CC   binding partner does not comprise TSH or naturally produced antibodies to
CC   the TSH receptor; and (4) a combination comprising the binding partner
CC   and one or more further agents capable of stimulating thyroid tissue,
CC   and/or tissue containing a TSH receptor, for simultaneous, separate or
CC   sequential use in stimulating thyroid tissue, and/or tissue containing a
CC   TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC   gene therapy. The polypeptide, compositions and methods from the present
CC   invention can be used for treating an autoimmune disease associated with
CC   an immune reaction to a TSH receptor. The specific binding partner is
CC   useful for the manufacture of a medicament for stimulating thyroid tissue
CC   or tissue containing a TSH receptor, and for treating thyroid cancer.
CC   ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC   sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC   and VL domains given in ABP96751 to ABP96778, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 214 AA;

Query Match   79.7%; Score 516.5; DB 6; Length 214;
Best Local Similarity   80.8%; Pred. No. 5.6e-36;
Matches   97; Conservative   11; Mismatches   11; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        :||||||||||||||||||||:|||||||:||||:||||:|||:|||||||||||:|||
Db   1 DVQLVQSGPELVKPGASVKMSCKASGYSFTGYNMHWVKQSHGESLEWIGYIDPYNGATSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAARGNF-PYYFDYWGQGTTLTVSS 119
        ||||||||||||||||||||||:||||||||||||||||||| ::||||
Db   61 SQKFKGKATLTVDKSSSTAYMHL

```
Db     61 NQKPEDKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARRWDWDPYAMDYWGQGTSVTVSS 120
```

```
RESULT 15

ABP96755

ID    ABP96755 standard; protein; 214 AA.
XX
AC    ABP96755;
XX
DT    05-JUN-2003 (first entry)
XX
DE    TSH receptor antibody 16E5 heavy chain amino acid sequence.
XX
KW    Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW    autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW    gene therapy; immune reaction; thyroid cancer.
XX
OS    Synthetic.
XX
XX
PN    WO200301B632-A2.
XX
PD    06-MAR-2003.
XX
PF    21-AUG-2002; 2002WO-GB003831.
XX
PR    23-AUG-2001; 2001GB-00020649.
PR    01-JUL-2002; 2002GB-0015212.
XX
PA    (RSRR-) RSR LTD.
XX
PI    Smith BR, Furmaniak J, Sanders JF;
XX
DR    WPI; 2003-290051/28.
DR    N-PSDB; ACC44910.
XX
PT    New polypeptide sequence having part or all of the primary structural
PT    conformation of one or more TSH receptor epitopes, useful for treating an
PT    autoimmune disease associated with an immune reaction to a TSH receptor,
PT    e.g. thyroid cancer.
XX
PS    Claim 71; Fig 13; 196pp; English.
XX
CC    The present invention describes a polypeptide sequence comprising part or
CC    all of the primary structural conformation of one or more thyrotropin
CC    (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC    produced in response to a TSH receptor interact. Also described: (1) one
CC    or more receptor TSH epitopes with which the autoantibodies and/or
CC    lymphocytes interact, as with the polypeptide sequence described above;
CC    (2) a method of screening for autoantibodies or lymphocytes produced in
CC    response to a TSH receptor in a sample of body fluid obtained from a
CC    subject suspected of suffering from, susceptible to, having or recovering
CC    from autoimmune disease associated with an immune reaction to a TSH
CC    receptor; (3) a binding partner for a TSH receptor, which is capable of
CC    binding to a TSH receptor to stimulate the TSH receptor, where the
CC    binding partner does not comprise TSH or naturally produced antibodies to
CC    the TSH receptor; and (4) a combination comprising the binding partner
CC    and one or more further agents capable of stimulating thyroid tissue,
CC    and/or tissue containing a TSH receptor, for simultaneous, separate or
CC    sequential use in stimulating thyroid tissue, and/or tissue containing a
CC    TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC    gene therapy. The polypeptide, compositions and methods from the present
CC    invention can be used for treating an autoimmune disease associated with
CC    an immune reaction to a TSH receptor. The specific binding partner is
CC    useful for the manufacture of a medicament for stimulating thyroid tissue
CC    or tissue containing a TSH receptor, and for treating thyroid cancer.
CC    ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC    sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC    and VL domains given in ABP96751 to ABP96778, which are used in the
CC    exemplification of the present invention
XX
SQ    Sequence 214 AA;
```

```
Qy     1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
         :::||:||||||||||||||||:|||||:|||||  :||| |::|||||||||| |:|||
Db     1 DVQLVQSGPELVKPGASVKMSCKASGYSFTGYNMHWVKQSHGKSLEWIGYIDPYNGATSY 60

Qy    61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNF-PYYFDYWGQGTTLTVSS 119
         :::|| |||||||||||||||:||||||||||||||||||||  :||:||||||||||||
Db    61 NQKFEDKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARRWDWDPYAMDYWGQGTSVTVSS 120
```

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OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 16.323 Seconds
                                         (without alignments)
                                         701.451 Million cell updates/sec

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Title: US-10-774-076-2
Perfect Score: 648
Sequence: 1 EIQLQQSGPELVKPGASVKV...........GNFPYYFDYWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Database :   PIR_79:*
             1:   pir1:*
             2:   pir2:*
             3:   pir3:*
             4:   pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	DB ID	Description
1	526.5	81.2	137	2	H32513	Ig heavy chain pre
2	518.5	80.0	119	2	F30502	Ig heavy chain V r
3	507.5	78.3	128	2	S20502	Ig heavy chain V r
4	505.5	78.0	128	2	S37267	Ig heavy chain V r
5	503.5	77.7	139	2	C37267	Ig heavy chain V r
6	499	77.0	121	2	A27609	Ig heavy chain pre
7	496	76.5	117	2	F37266	Ig heavy chain V r
8	496	76.5	117	2	S03305	Ig heavy chain V r
9	493	76.1	117	1	MHMS4B	Ig heavy chain V r
10	493	76.1	140	2	T01407	Ig heavy chain (my
11	491.5	75.8	128	2	A37267	Ig heavy chain V r
12	490.5	75.7	150	2	PN0444	Ig heavy chain V r
13	485	74.8	117	1	MHMSJ5	Ig heavy chain V r
14	483	74.5	121	2	H37266	Ig heavy chain V r
15	481	74.2	118	2	PL0200	Ig anti-DNA autoantib
16	476.5	73.5	122	2	PH0887	Ig heavy chain V r
17	475.5	73.4	135	2	PS0057	Ig heavy chain V r
18	475	73.3	107	2	PH0971	Ig heavy chain pre
19	474.5	73.2	118	2	S38717	Ig heavy chain V r
20	473.5	73.1	112	2	S09957	Ig heavy chain V-D
21	470.5	72.6	117	2	S25176	Ig heavy chain V r
22	469	72.4	119	2	PH0099	Ig heavy chain V r
23	468.5	72.3	114	2	S26319	Ig heavy chain V r
24	468.5	72.3	120	2	E45722	Ig anti-glycoprotein
25	466	71.9	117	2	S01822	Ig heavy chain V-D
26	466	71.9	119	2	B53285	Ig heavy chain V a
27	465	71.8	119	2	PL0011	Ig heavy chain V r
28	465	71.8	151	2	PL0011	Ig heavy chain pre
29	464	71.6	138	2	PH0105	Ig heavy chain V r
30	464	71.6	118	2	MHMS38	Ig anti-digoxin trans
31	463.5	71.5	118	1	MHMS38	Ig heavy chain V r
32	463	71.5	166	2	PL0012	Ig heavy chain pre

30	460	71.0	118	2	S38565	Ig heavy chain V r
31	459.5	70.9	120	2	A49982	Ig heavy chain V r
32	459.5	70.9	122	2	B37267	Ig heavy chain V r
33	457	70.5	119	2	S20640	Ig heavy chain V r
34	456.5	70.4	120	2	B22769	Ig heavy chain V r
35	455.5	70.3	108	2	PH0972	Ig heavy chain V r
36	455.5	70.3	120	2	F45722	Ig anti-glycoprotein
37	452	69.8	113	2	PH0974	Ig heavy chain V r
38	452	69.8	136	1	HVMSB1	Ig heavy chain pre
39	451.5	69.7	108	2	PH0975	Ig heavy chain V r
40	451.5	69.7	116	2	S53751	antibody Fab Jel 1
41	451.5	69.7	118	2	PL0084	Ig heavy chain V r
42	450.5	69.5	139	1	MHMS18	Ig heavy chain V r
43	450.5	69.5	287	4	PC4402	pelB leader/Ig hea
44	450	69.4	109	2	PH0973	Ig heavy chain V r
45	450	69.4	117	1	HVMS8A	Ig heavy chain pre

ALIGNMENTS

RESULT 1
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: GB:M208311; NID:g196949; PIDN:AAA38848.1; PID:g196950
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   81.2%; Score 526.5; DB 2; Length 137;
Best Local Similarity 84.9%; Pred. No. 1.9e-39;
Matches 101; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
           ||||||||||||||||||||||||||||||| ||| |||||||||||||| :|:|||| |
Db   20 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYYGSTSY 79

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
           :|||||||||||||||||||| |||||||||||||||| | |:|||||||||||| |
Db   80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARK-NYGSSFDYWGQGTTLTVSS 137

RESULT 2
F30502
Ig heavy chain V region (A52) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: F30502
R;Bilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mi...
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: F30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <BIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   80.0%; Score 518.5; DB 2; Length 119;
Best Local Similarity 82.8%; Pred. No. 8.2e-39;
Matches 101; Conservative 5; Mismatches 9; Indels 7; Gaps 2;

Left column

```
Qy    1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDGY 60
          |||||||| |||||||||| ||||||| ||  ||| |||||||||||||||:|||||:
Db    1 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGKINPYYGSTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCA----RRGNFPYFDYWGQGTTLT 116
          :||||||||||||||||||||:||||||||||||||    |||   :YFDYWGQGTTLT
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGRLRRGG---YFDYWGQGTTLT 117

Qy  117 VS 118
          ||
Db  118 VS 119
```

RESULT 3
I37267
Ig heavy chain V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: I37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: I37267
A;Molecule type: mRNA
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-128 <RUF>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```
Query Match             79.3%;  Score 507.5;  DB 2;  Length 128;
Best Local Similarity   79.7%;  Pred. No. 8.2e-38;
Matches 98;  Conservative 5;  Mismatches 15;  Indels 5;  Gaps 1;

Qy    2 IQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDGYS 61
          ||||||| |||||||||| ||||||| ||  ||| |||||||||||||||:|||||:
Db    6 VQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGYSYN 65

Qy   62 QKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRG----NFPYFDYWGQGTTLT 116
          ||||||||||||||||||||||||||||||||||||||    : |||||||||||||
Db   66 QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGLTVVAKSYYFDYWGQGTTLT 125
```

RESULT 4
C37267
Ig heavy chain V region (Py69) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: C37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: C37267
A;Molecule type: mRNA
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-128 <RUF>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```
Query Match             78.0%;  Score 505.5;  DB 2;  Length 128;
Best Local Similarity   78.0%;  Pred. No. 1.2e-37;
Matches 96;  Conservative 7;  Mismatches 15;  Indels 5;  Gaps 1;

Qy    2 IQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDGYS 61
          |||||||||||||||||| |||||||| ||  ||| |||||||||||||||:|||::||
Db    6 VQLQQSGPELVKPGASVKISCKTSGYTFTNYNMYWVKQSHGKSLEWIGYIDPYGDPGYS 61

Qy   62 QKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDGYS 61
```

Right column

```
Db    6 VQLQQSGPELVKPGASMKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGRFNPNSGGSTYN 65

Qy   62 QKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNF------PYYFDYWGQGTTLT 116
          ||||||||||||||||||||  |||||||||||||||||:      . : |||||||||
Db   66 QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGPYGNYYSYYFDYWGQGTTLT 125

Qy  117 VSS 119
          |||
Db  126 VSS 128
```

RESULT 5
A27609
Ig heavy chain precursor V region (I29) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
C;Genetics:
A;Introns: 16/1
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology <IMM>

```
Query Match             77.7%;  Score 503.5;  DB 2;  Length 139;
Best Local Similarity   80.0%;  Pred. No. 2e-37;
Matches 96;  Conservative 10;  Mismatches 13;  Indels 1;  Gaps 1;

Qy    1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDGY 60
          :||||||||||||||||| |||||| || |||| |||||||||||||||||:|||:
Db    1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYVMHWVKQSNGKSLEWIGYINPYNDYTSY 79

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYY-FDYWGQGTTLTVSS 119
          :||||||||||||||||||||  |||||||||||||||||   | |||||||||::|||
Db   80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARYSYSYYAMDYWGQGTSVTVSS 139
```

RESULT 6
P37266
Ig heavy chain V region (Py2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: P37266
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: P37266
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-121 <RUF>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-100/Domain: immunoglobulin homology <IMM>

```
Query Match             77.0%;  Score 499;  DB 2;  Length 121;
Best Local Similarity   81.4%;  Pred. No. 4.3e-37;
Matches 96;  Conservative 8;  Mismatches 12;  Indels 2;  Gaps 1;

Qy    1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDGY 60
          :|||||||||||||||| |||| || || |||| |||||||||||||||||:|||:
Db   20 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYVMHWVKQSNGKSLEWIGGINPNSG--GTN 63

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYY-FDYWGQGTTLTVSS 119
          :|||||||||||||||||||| |||||||||||||||||   : | :||||||||::|||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARYSYSYYAMDYWGQGTSVTVSS 119

Qy    2 IQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDGYS 61
          |||||||||||||||||| |||||||| || |||| |||||||||||||||:|||::|
Db    6 VQLQQSGPELVKPGASVKISCKTSGYTFTEYIIHWVKQSHGKSLEWIGGINPNSG--GTN 63

Qy   62 QKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
```

RESULT 7
S03305
Ig heavy chain V region (6B12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: JL0044; S05276; S03305
R;Van Cleve, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A;Title: Do antibodies recognize amino acid side chains of protein antigens independentl
A;Reference number: JL0043; MUID:88258372; PMID:2455014
A;Accession: JL0044
A;Molecule type: mRNA
A;Residues: 1-117 <VAN>
A;Cross-references: EMBL:X12381
R;Metzger, D.W.
submitted to the EMBL Data Library, July 1988
A;Reference number: S05276
A;Accession: S05276
A;Molecule type: mRNA
A;Residues: 1-116, 'I' <MET>
A;Cross-references: EMBL:X12381; NID:g52094; PIDN:CAA30939.1; PID:g930170
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match　　　76.5%; Score 496; DB 2; Length 117;
Best Local Similarity　80.7%; Pred. No. 7.7e-37;
Matches 96; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

Qy　　1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIYPYGDPGY 60
　　　　 ::|||||||||||| |||||| |||||||||||| || |||||||||||| ||||||
Db　　1 EVQLQQSGPEAGKPGASVKMSCKASGYTFTDYYINWVKQSHGKSLEWIGYIYPNIDETAY 60

Qy　61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGRNPPYYFDYWGQGTTLTVSS 119
　　　 ||||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||
Db　61 SQKFKGKATLTVDKSSSTAYMELRSLTSDDSAVYYCARRN--VYFDYWGQGTTLTVSS 117

RESULT 8
MHMS4E
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A02039
R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain co
A;Reference number: A02039; MUID:83075344; PMID:6816276
A;Accession: A02039
A;Molecule type: protein
A;Residues: 1-117 <KEH>
A;Cross-references: UNIPROT:P01756
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context a
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted
F;55/Binding site: carbohydrate (Asn) (covalent) #status atypical

Query Match　　　76.1%; Score 493; DB 1; Length 117;
Best Local Similarity　79.8%; Pred. No. 1.4e-36;
Matches 95; Conservative 9; Mismatches 13; Indels 2; Gaps 1;

Qy　　1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIYPYGDPGY 60
　　　　 :|||||||||||||||||||| |||||| ||| || |||||||||||||||||| |:|
Db　　1 EVQLQQSGPELVKPGASVRMSCKASGYTFTDYYMKVWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy　61 SQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
　　　 ||||||||||||||||||||| ||||||||||||||||| |||||||||||||||||
Db　61 NQRFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR----GPYGNYNNSYYFDYWGQGTTL 124

RESULT 9
T01407
Ig heavy chain V region (myeloma M104B) - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C;Accession: T01407
R;Takahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamano
Microbiol. Immunol. 36, 855-863, 1992
A;Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic an
A;Reference number: Z14317; MUID:93116638; PMID:1474935
A;Accession: T01407
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-140 <TAK>
A;Cross-references: EMBL:S51851; NID:g262657
A;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match　　　76.1%; Score 493; DB 2; Length 140;
Best Local Similarity　79.8%; Pred. No. 1.7e-36;
Matches 95; Conservative 9; Mismatches 13; Indels 2; Gaps 1;

Qy　　1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIYPYGDPGY 60
　　　　 :|||||||||||||| |||||| |||||| ||| |:| |||||||||||||||| ||||
Db　20 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYINWVKQSHGKSLEWIGYIYPNIDETAY 79

Qy　61 SQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
　　　 |||||||||||||||||||||||||| |||||||||||||| |||||||||||||||||
Db　80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DYDWYFDVWGAGTTVTVSS 136

RESULT 10
A37267
Ig heavy chain V region (Py20) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: A37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of ant
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match　　　75.8%; Score 491.5; DB 2; Length 128;
Best Local Similarity　75.8%; Pred. No. 2.1e-36;
Matches 94; Conservative 9; Mismatches 16; Indels 5; Gaps 1;

Qy　　1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIYPYGDPGY 60
　　　　 :|||||||||||||| |||||| |||||||||||||| :|.| |||||||||||| :|
Db　　5 EVQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWMGGINPNSGGTRD 64

Qy　61 SQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGNP-----PYYFDYWGQGTTL 115
　　　 ||||||||||||||||||||| |||||||||||||||||| |||||||||||||
Db　65 NQRFKGKATLTVDKSSIAYMELRSLTSEDSAVYYCARRGPYGNYYNSYYFDYWGQGTTL 124

RESULT 11
PN0444
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0444
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymera...
A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0444
A;Molecule type: mRNA
A;Residues: 1-150 <KAL>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
A;Title: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Product: Ig heavy chain V region #status predicted <MAT>
F;20-150/Product: Ig heavy chain V region #status predicted <MAT>
F;20-117/Domain: variable region <VRG>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   75.7%; Score 490.5; DB 2; Length 150;
Best Local Similarity   78.2%; Pred. No. 3e-36;
Matches   93; Conservative   9; Mismatches   16; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
Db   20 EVQLQQFGAELVKPGTSVKISCKASGYIFFDYNMDWVKQSHGKSLEWIGDIDPNFDSSSY 79

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
Db   80 NQKFKGKATLTVDKSSNTAYMELRSLTSEDTAVYYCA-RGGFPYGMDYWCGTSVTVSS 137

RESULT 12
MHMS25
Ig heavy chain V region (J558) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
Nature 283, 35-40, 1980
A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
A;Reference number: A26242; MUID:80078170; PMID:6765983
C;Accession: A26242
A;Molecule type: protein
A;Residues: 1-117 <SCH>
A;Cross-references: UNIPROT:P01757
A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that ...
C;Comment: This protein binds dextran.
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

Query Match   74.8%; Score 485; DB 1; Length 117;
Best Local Similarity   79.8%; Pred. No. 7.1e-36;
Matches   95; Conservative   8; Mismatches   14; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DRVWYFDVWGAGTTVTVSS 117

RESULT 13
H37266
Ig heavy chain V region (Py54) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti...
A;Reference number: A38740; MUID:91177923; PMID:1706720
C;Accession: H37266
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-121 <RUF>
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-100/Domain: immunoglobulin homology <IMM>

Query Match   74.5%; Score 483; DB 2; Length 121;
Best Local Similarity   79.7%; Pred. No. 1.1e-35;
Matches   94; Conservative   8; Mismatches   14; Indels   2; Gaps   1;

Qy   2 IQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGYS 61
Db   6 VQLQQSGPELVKPGASVKISCKSCKTFGYTFTEYIIHWVKQSPGKSLEWIGGINPNSG-- 63

Qy   62 QKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
Db   64 QKFRGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGDNLYYFDVWGQGTTLTVSS 121

RESULT 14
PL0200
anti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Reference number: PL0198; MUID:9030768; PMID:2114528
A;Accession: PL0200
A;Reference: Variable region primary structures of monoclonal anti-DNA autoantibodies from M...
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
C;Accession: PL0200
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
A;Cross-references: GB:X53641; NID:g50193; PIDN:CAA37692.1; PID:g930139
A;Molecule type: protein
A;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;50-66/Region: complementarity-determining 2
F;99-110/Region: complementarity-determining 3
F;99-106/Region: D region
F;107-118/Region: JH region

Query Match   74.2%; Score 481; DB 2; Length 118;
Best Local Similarity   78.8%; Pred. No. 1.6e-35;
Matches   93; Conservative   8; Mismatches   15; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
Db   1 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYYGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAR--RGNFPYYFDYWGQGTTLT 116
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGITYTSTRTWFPAYWGQGTLVT 118

RESULT 15
PH0887
Ig heavy chain V region (anti-CD3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0887
A;Molecule type: mRNA
A;Residues: 1-122 <SHA>
R;Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann,
J. Exp. Med. 175, 217-225, 1992
A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocy...
A;Reference number: PH0885; MUID:92113462; PMID:1346155
A;Accession: PH0887
A;Note: the authors translated the codon TTC for residue 70 as Leu
C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-98/Domain: immunoglobulin homology <IMM>

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Query Match         73.5%;   Score 476.5;  DB 2;   Length 122;
Best Local Similarity  74.6%;   Pred. No. 4.1e-35;
Matches  91;  Conservative  11;  Mismatches  17;  Indels  3;  Gaps  1;

Qy    1  EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY  60
            |:||||||||||||||||||:||||||||| | ||||||||||:||:|||||||||
Db    1  EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYYKGVSTY  60

Qy   61  SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNF---PYYFDYWGQGTTLTV 117
            :||||| | ||||||||||||||||||||||||||||||  :   |||||| |||||:||
Db   61  NQKFKDKATFTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 120

Qy  118  SS 119
            || ||
Db  121  SS 122
```

Search completed: December 29, 2004, 18:06:55
Job time : 17.4897 secs

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: December 29, 2004, 17:38:43 ; Search time 82.1416 Seconds
(without alignments)
833.556 Million cell updates/sec

Title:
Perfect Score: 648
Sequence: 1 EIQLQQSGPELVKPGASVKV..........GNFPYYFDYWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	509	78.5	117	2	Q90XF0	q90xf0 mus musculu
2	501	77.3	470	2	Q7TMK1	q7tmk1 mus musculu
3	500	77.2	120	2	Q99125	q99125 mus musculu
4	499	77.0	472	2	Q920E8	q920e8 mus musculu
5	499	77.0	472	2	Q6PJA7	q6pja7 mus musculu
6	493	76.1	117	2	AAH18535	aah18535 mus muscu
7	491	75.8	123	2	HV12_MOUSE	p01756 mus musculu
8	489.5	75.5	481	2	Q8VIJ1	q8vij1 mus musculu
9	485	74.8	117	2	Q8VCV5	q8vcv5 mus musculu
10	485	74.8	117	2	HV13_MOUSE	p01757 mus musculu
11	469.5	72.5	488	2	Q9QXE9	q9qxe9 mus musculu
12	463.5	71.5	118	2	Q91WR1	q91wr1 mus musculu
13	462	71.3	146	2	HV51_MOUSE	p06330 mus musculu
14	454	70.1	170	2	Q924R8	q924r8 mus musculu
15	452	69.8	136	2	Q925S2	q925s2 mus musculu
16	450.5	69.5	139	2	HV15_MOUSE	p01759 mus musculu
17	450.5	69.5	145	2	HV07_MOUSE	p01751 mus musculu
18	450	69.4	117	2	Q924Q7	q924q7 mus musculu
19	447.5	69.1	465	2	HV14_MOUSE	p01758 mus musculu
20	447.5	69.1	465	2	Q6PJB2	q6pjb2 mus musculu
21	447.5	69.1	488	2	AAH18280	aah18280 mus muscu
22	447	69.0	120	1	Q8KOF2	q8k0f2 mus musculu
23	444	68.5	144	2	HV03_MOUSE	p01747 mus musculu
24	444	68.5	145	2	Q924P5	q924p5 mus musculu
25	440.5	68.0	145	2	Q924R4	q924r4 mus musculu
26	439.5	67.8	109	2	Q9JL75	q9jl75 mus musculu
27	439.5	67.8	145	2	Q924R6	q924r6 mus musculu
28	438.5	67.7	145	2	Q924Q6	q924q6 mus musculu
29	438.5	67.7	142	2	Q924R1	q924r1 mus musculu
30	438	67.6	142	2	Q924Q1	q924q1 mus musculu
31	437.5	67.5	143	2	Q924R7	q924r7 mus musculu
32	437.5	67.5	145	2	Q924Q9	q924q9 mus musculu
33	437.5	67.5	145	2	Q924R3	q924r3 mus musculu
34	437.5	67.5	473	2	Q99125	q99125 mus musculu
35	437.5	67.5	482	2	Q8K172	q8k172 mus musculu
36	436.5	67.4	145	2	Q924P7	q924p7 mus musculu
37	436	67.3	614	2	Q7TMT6	q7tmt6 mus musculu
38	434.5	67.1	143	2	Q924Q5	q924q5 mus musculu
39	434.5	67.1	143	2	Q924R0	q924r0 mus musculu
40	434	67.0	140	1	HV02_MOUSE	p01746 mus musculu
41	433	66.8	146	2	Q91VA2	q91va2 mus musculu
42	432.5	66.7	143	2	Q924Q0	q924q0 mus musculu
43	432.5	66.7	143	2	Q924Q3	q924q3 mus musculu
44	432	66.7	140	2	Q924R2	q924r2 mus musculu
45	432	66.7	146	2	Q924Q8	q924q8 mus musculu

ALIGNMENTS

RESULT 1
Q90XF0
ID   Q90XF0;   PRELIMINARY;   PRT;   117 AA.
AC   Q90XF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   PIR; PH0973; PH0973.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match   78.5%; Score 509; DB 2; Length 117;
Best Local Similarity 83.2%; Pred. No. 6.2e-43;
Matches   99; Conservative 6; Mismatches 12; Indels 2; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
         |:|||||||||||||||||||:||||:||||||||||||||||||||||||:|||||
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
         ||||||||||||||||||||| |||||||||||||||| ||||||||||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DKDYYFDYWGQGTTLTVSS 117

RESULT 2
Q7TMK1
ID   Q7TMK1;   PRELIMINARY;   PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;

RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RX   MEDLINE=22388257; PubMed=12477932;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RL   "Generation and initial analysis of more than 15,000 full-length human
RL   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
SQ   SEQUENCE FROM N.A.
SQ   SEQUENCE FROM N.A.

Qy   Query Match   77.3%;   Score 501; DB 2; Length 470;
     Best Local Similarity 78.7%;   Pred. No. 1.9e-41;
Db   Matches 96;   Conservative 10; Mismatches 12; Indels 4; Gaps 2;

Qy   1 EIQLQQSGGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 20 EVQLQQSGGPELVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY 79

Qy 61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVVYCAR----RGNPFYYFDYWGQGTTLTV 117
        |||||||||||||||||||||| ||||||||||||||| |||| ||||||||||||||
Db 80 NQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARYYSGSY-WYFDVWGAGTTVTV 138

Qy 118 SS 119
         ||
Db 139 SS 140

RESULT 3
ID   Q92OE8
AC   Q92OE8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Pterin-mimicking anti-idiotope heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).

RESULT 3
Q92OE8

ID   Q92OE8   PRELIMINARY;   PRT;   120 AA.

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
OX   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307936; AAL09420.1; -.
HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVVYCAR----RGNPFYYFDYWGQGTTLTV 118
         ||||||||||||||| ||||||||||||||||| |||| ||||||||||||||||
Db   1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYYMNWVKQSGNGKSLEWIGNIDPYVGGTSY 60

Qy   61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVVYCAVIYYGNSPAWFAYWGQGTLVTVS 120

RESULT 4
Q6PJA7

ID   Q6PJA7   PRELIMINARY;   PRT;   472 AA.
AC   Q6PJA7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RL   "Generation and initial analysis of more than 15,000 full-length human
RL   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

Qy   Query Match   77.2%;   Score 500; DB 2; Length 120;
     Best Local Similarity 80.0%;   Pred. No. 5e-42;
Db   Matches 96;   Conservative 7; Mismatches 15; Indels 2; Gaps 1;

Qy   1 EIQLQQSGGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
        |||||||||| ||||||||| ||||||| | ||||||||||||||||| |||||||
Db   1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYYMNWVKQSGNGKSLEWIGNIDPYVGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVVYCA----RRGNPFYYFDYWGQGTTLTVS 118
         |||||||||||||||||||||| |||||||||||| |:| |||||||||||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVVYCAVIYYGNSPAWFAYWGQGTLVTVS 120

RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018535; AAH18535.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA; 52299 MW; 165169C23D55D4AB CRC64;

Query Match   77.0%; Score 499; DB 2; Length 472;
Best Local Similarity   78.0%; Pred. No. 3.1e-41;
Matches   96; Conservative   10; Mismatches   13; Indels   4; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |:||||||||||||||||||||||||||||||||:|:||:|:|:||||||||||:|||||
Db   20 EVQLQQSGPELVKTGASVKMSCKASGYTFSDYYMHWVKQSHGKSLEWIGYIYPNNGGNGY 79

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAR----RGNPFYYFDYWGQGTTLT 116
          :|||||||||||||||||||||||||||||||||||| :||||||||:||||||||:|
Db   80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGYISYYSYDHYFDYWGQGTTIT 139

Qy   117 VSS 119
          |||
Db   140 VSS 142

RESULT 5
ID   AAH18535   PRELIMINARY;   PRT;   472 AA.
AC   AAH18535;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarstne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]

RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018535; AAH18535.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA; 52299 MW; 165169C23D55D4AB CRC64;

Query Match   77.0%; Score 499; DB 2; Length 472;
Best Local Similarity   78.0%; Pred. No. 3.1e-41;
Matches   96; Conservative   10; Mismatches   13; Indels   4; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          |:||||||||||||||||||||||||||||||||:|:||:|:|:||||||||||:|||||
Db   20 EVQLQQSGPELVKTGASVKMSCKASGYTFSDYYMHWVKQSHGKSLEWIGYIYPNNGGNGY 79

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAR----RGNPFYYFDYWGQGTTLT 116
          :|||||||||||||||||||||||||||||||||||| :||||||||:||||||||:|
Db   80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGYISYYSYDHYFDYWGQGTTIT 139

Qy   117 VSS 119
          |||
Db   140 VSS 142

RESULT 6
ID   HV12_MOUSE   STANDARD;   PRT;   117 AA.
HV12_MOUSE
AC   P01751;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V region MOPC 104E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX   MEDLINE=83075344; PubMed=6812276;
RA   Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA   Hood L.E.;
RT   "Complete amino acid sequence of a mouse mu chain: homology among
RT   heavy chain constant region domains.";
RL   Biochemistry 21:5415-5424(1982).
RN   [1]
CC   -!- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma
CC   protein has also been determined.
CC   -!- MISCELLANEOUS: This protein binds dextran.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02039; MHMS4E.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
FT   DOMAIN   1   116   Ig-like.
FT   DISULFID   22   96   By similarity.
FT   CARBOHYD   55   55   N-linked (GlcNAc...) (complex).
NON_TER   117   117
SQ   SEQUENCE   117 AA; 12983 MW; 3CF8ACE4BB447B41 CRC64;

Query Match   76.1%; Score 493; DB 1; Length 117;
Best Local Similarity   79.8%; Pred. No. 2.4e-41;
Matches   95; Conservative   9; Mismatches   13; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          :|||||||||||||:||||||||||||||:||:||:|:|:||||||||||||:|:||||||
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
          :||||||||||||||||||||||||||||||||||||||||:||||:||||||||||||

Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DYDWYFDVWGAGTTVTVSS 117

RESULT 7

ID   Q8VIJ1   PRELIMINARY;   PRT;   123 AA.
AC   Q8VIJ1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-DNA heavy chain (Fragment).
GN   Name=J558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H/HeJ-lpr/lpr;
RX   MEDLINE=9640928; PubMed=8814271;
RA   Bloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT   "Differences in V kappa gene utilization and VH CDR3 sequence among
RT   anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL   Eur. J. Immunol. 26:2225-2233(1996).
DR   EMBL; U59154; AAB02916.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   123   123
SQ   SEQUENCE   123 AA; 13806 MW; CC0037A806E9911E CRC64;

Query Match   75.8%; Score 491; DB 2; Length 123;
Best Local Similarity   76.8%;
Matches 96; Conservative   8; Mismatches 13; Indels   8; Gaps   2;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          ||||||||||||||||:|||||||||||||||: |||||||||||||||||||||||||
Db   1 EIQLQQSGTELVKPGASVKISCKASGYSFTGYNMAWVKQSHGKSLEWGDINPYYGGTRY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYY------PDYWGQGTT 114
          |||||||||||||||||||| |||||||||||||||||||| || ||||||||
Db   61 SQKFDKDATLTVDKSSRTAYMQLNSLTSEDSAVYYCAR--DYTYTYDEGCFAVWGQGTL 118

Qy   115 LTVSS 119
          :||:
Db   119 VTVSA 123

RESULT 8

ID   Q8VCV5   PRELIMINARY;   PRT;   481 AA.
AC   Q8VCV5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N;
RC   TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N;
RC   TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018455; AAH18455.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; IGv; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   481 AA; 52326 MW; 52B44C582680714 3 CRC64;

Query Match   75.5%; Score 489.5; DB 2; Length 481;
Best Local Similarity   76.5%;
Matches 91; Conservative 14; Mismatches 13; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          ||||||||||||||||:|||||||||||||||: |||||||||||||||||||||||||
Db   20 EIQLQQSGPELVRPGTSVKVSCKASGYSFTDYNIYWVKQSHGKSLEWIGYIDPYNGGSSY 79

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNFPYYFDYWGQGTTLTVSS 119
          |||||||||||||||||||||||||||||||||||||||| :| ||||||||||:||:
Db   80 NQKFKGKATLTVDKSSNTAFMYLNNLTSEDSAFYYCAREW-YGAWFAFWGQGTLVTVSA 137

RESULT 9

ID   HV13_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
CC   bind dextran differ from that shown at 1-7 positions, many of
CC   which occur in the D and J segments.
CC   -!- MISCELLANEOUS: This protein binds dextran.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A26242; MHMSJ5.

DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN   1   116
FT   DISULFID   22   96   By similarity.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 13024 MW; 292E2AF4BB447E41 CRC64;

Query Match   74.8%; Score 485; DB 1; Length 117;
Best Local Similarity   79.8%; Conservative   8; Mismatches   14; Indels   2; Gaps   1;
Matches 95;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
               :|||||||||||||||||||||:|||||||| ||||||||||||||||||||| |||||
Db   1 EVQLQQSGPELVKPGASVKVSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
               :|||||||||||||||||||:||||||||||||||||||| |||||||||||:||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DRYWYFDVWGAGTTVTVSS 117

RESULT 10
ID   Q9QXE9
AC   Q9QXE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ225174; CAB65237.1; -.
PIR; F33932; F33932.
HSSP; P01751; 1NQB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER   1   1
NON_TER   117   117
SEQUENCE   117 AA; 13000 MW; CDDE2AF84D49734 CRC64;

Query Match   74.8%; Score 485; DB 2; Length 117;
Best Local Similarity   79.8%; Pred. No. 1.5e-40; Mismatches   14; Indels   2; Gaps   1;
Matches 95; Conservative   8;

Qy   1 EIQLQQSGPELVKPGASVKVSCKAGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
               :||||||||||||||||||||:|||||||| ||||||||||||||||||||| |||||
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
               :|||||||||||||||||||:||||||||||||||||||| |||||||||||:||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DRYWYFDVWGAGTTVTVSS 117

DE   Igh-VJ558 protein.
GN   Name=Igh-VJ558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013539; AAH13539.1; -.
HSSP; P01751; 1A6W.
MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003008; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 2.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SEQUENCE   488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match   72.5%; Score 469.5; DB 2; Length 488;
Best Local Similarity   73.4%; Pred. No. 2.8e-38; Mismatches   17; Indels   5; Gaps   1;
Matches 91; Conservative 11;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
               :||||||||||||||||||||:|||||||| ||||||||||||||||||||| |||||
Db   20 EVQLQQSGPELVKPGASVKLSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 79

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFYYF-----DYWGQGTTL 115
               :|||||||||||||||||||:|||||||||||||||||||| |||| ||||||||
Db   80 NQKFKGKATLTVDKSSSTAYMQLNNLTSDDSAVYYCARGPVYYSYFSYDRGDYWGQGTLV 139

RESULT 11
ID   Q91WR1
AC   Q91WR1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

RESULT 12
ID   HV51_MOUSE
AC   P06330;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)

Query Match   74.8%; PRELIMINARY; PRT; 488 AA.
Best Local Similarity   79.8%; Pred. No. 1.5e-40; Mismatches   14; Indels   2; Gaps   1;
Matches 95; Conservative   8;

Qy   1 EIQLQQSGPELVKPGASVKVSCKAGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
               :|||||||||||||||||||||:|||||||| ||||||||||||||||||||| |||||
Db   1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRGNPFYYFDYWGQGTTLTVSS 119
               :|||||||||||||||||||:||||||||||||||||||| ||||||||||:||||||
Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCAR--DRYAMDYWGQGTSVTVSS 117

Qy   116 TVSS 119
               |||
Db   140 TVSA 143

DE   Ig heavy chain V region AC38 205.12.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02040; MMS38.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN   1   98   V segment.
FT   DOMAIN   99   104   D segment.
FT   DOMAIN   105   118   J segment.
FT   DISULFID   22   96   By similarity.
FT   NON_TER   118   118
SQ   SEQUENCE   118 AA; 12934 MW; 94F7BEE4C7622A018 CRC64;

Query Match   71.5%; Score 463.5; DB 1; Length 118;
Best Local Similarity   77.5%; Pred. No. 2.2e-38;
Matches 93; Conservative 6; Mismatches 18; Indels 3; Gaps 2;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY   60
         :|||||||||||||||||||:||||||| :| :| :||||||||||||||||:||||
Db   1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY   60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAR-RGNFPYYFDYWGQGTTLTVSS 119
         :|||||||||||||||||| | | | |||||||||||| ||:: :||:|| |||:|||
Db   61 NQKFKGKATLTVDKSSSATVMELRSLTSEDSAVYYCARGYGDP--FDVWGTGTTVTVSS   118

RESULT 13
ID   Q924R8   PRELIMINARY;   PRT;   146 AA.
AC   Q924R8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH186.2-D-J-C mu protein (Fragment).
GN   Name=VH186.2-D-J-C mu;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Kozono Y., Kozono H., Azuma T.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB067781; BAB63266.1; -.
DR   PIR; F28833; F28833.
DR   PIR; PH1105; PH1105.
DR   PIR; PH1108; PH1108.
DR   PIR; PH1114; PH1114.
DR   PIR; PH1118; PH1118.
DR   PIR; PH1119; PH1119.
DR   PIR; PH1125; PH1125.
DR   PIR; PH1126; PH1126.
DR   PIR; PH1128; PH1128.
DR   PIR; PH1129; PH1129.
DR   PIR; PH1131; PH1131.
DR   PIR; PH1134; PH1134.
DR   PIR; PH1137; PH1137.
DR   PIR; PH1139; PH1139.
DR   PIR; PH1142; PH1142.
DR   PIR; PH1144; PH1144.
DR   PIR; PH1147; PH1147.
DR   PIR; PH1149; PH1149.
DR   PIR; PH1150; PH1150.
DR   PIR; PH1151; PH1151.
DR   PIR; PH1152; PH1152.
DR   PIR; PH1153; PH1153.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   146   146
SQ   SEQUENCE   146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;

Query Match   71.3%; Score 462; DB 2; Length 146;
Best Local Similarity   74.4%; Pred. No. 3.9e-38;
Matches 90; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY   60
         :||||| |||||||||||:||||||||||:|:| :|:|||||||||||||:||||||||
Db   1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY   60

Qy   61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARR--GNFPYYFDYWGQGTTLTVS 118
         :||||.||||||||.|||||||.| |||||||||||||| ||.||||||||||||||||
Db   61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARSYYGSSLYYFDYWGQGTTLTVS 120

RESULT 14
ID   Q92SS2   PRELIMINARY;   PRT;   170 AA.
AC   Q92SS2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MRP4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   PubMed=11819679;
RA   Cui D., Zeng G., Yan X., Li X., Su C.;
RT   "Cloning of mouse genes related to repairing of intestinal epithelium
RT   of the irradiated mice by treatment with the intestinal RNA of mice of
RT   the same strain.";
RL   Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA   Su C.;
RT   "Mechanism of exogenous nucleic acids and their precursors improving
RT   the repair of intestinal epithelium after irradiation in mice.";
RL   World J. Gastroenterol. 6:709-717(2000).
DR   EMBL; AF240167; AAK43732.1; -.
DR   HSSP; P01751; 1A6W.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match   70.1%; Score 454; DB 2; Length 170;

```
Best Local Similarity  68.0%; Pred. No. 2.9e-37;
Matches 83; Conservative 19; Mismatches 16; Indels 4; Gaps 2;

Qy      1 BIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          :::||||||:||:|:|:|||||||||||||||||||||||||||||||||||||||:|  |
Db      3 QVKLQQSGPEVVRPGVSVKISCKGSGYTFTDYSMHWLKMNHAQSLEWIGYIISTYDGNTNY 62

Qy     61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAR--RGNFPYYFPDYWGQGTTLTV 117
          :||||||||||||||||||| |||| ||||||||||||  |:|  ||||||||||||||:||
Db     63 NQKFKGKATMTVDKSSITAYMELARLTSDDSAIYYCARGAYYGSF-YYFDYWGQGTTVTV 121

Qy    118 SS 119
          ||
Db    122 SS 123
```

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RESULT 15
HV15_MOUSE
ID   HV15_MOUSE     STANDARD;      PRT;    136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig heavy chain V region BCL1 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.R.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared by
RT   two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    136       Ig heavy chain V region BCL1.
FT   DOMAIN       20    135       Ig-like.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15078 MW;  6827CFBC6DB3F35E CRC64;
```

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Query Match               69.8%;  Score 452; DB 1;  Length 136;
Best Local Similarity     72.5%;  Pred. No.3.6e-37;
Matches 87; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

Qy      1 BIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60
          :||||||:||:|:||||||||||||||:|||||||||||||||||||||||||:|  |
Db     20 QVKLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79

Qy     61 SQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAR-RGNFPYYFPDYWGQGTTLTVSS 119
          :||||||||||||||| ||||||||||||||||||| |:| |||||||||||||||||||||
Db     80 NQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCARYYGN---YFDYWGQGTTLTVSS 136
```